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February 28, 2003, 19:58:51; Search time 45.0389 Seconds (without alignments) 15700.357 Million cell updates/sec
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N. Zeineseg_101002;

SIDS2/gcgdata/geneseg/genesegn-embl_NR1981.DAT:*

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

14 : 114 : 115 : 120 : 1

SUMMARIES

		Description	Human partial card	Human adenylylcycl	Human cardiac aden	Human cardiac aden	Human modified car	Human type VI aden	Cardiac adenylyl c	Mouse ischaemic co	Type VI adenylyl c
	;	ID	AAD08561	AAV23246	AAD08563	AAD08567	AAD08568	AAX00461	AAQ42525	AB199680	AAA53923
		96	22	19	22	22	22	20	14	24	21
	Query	Length	314	2127	3549	3552	3582	4942	4046	5841	4131
æ	Query	Match	99.7	99.7	94.0	94.0	94.0	94.0	72.4	63.4	63.1
	,	score	313	313	295.2	295.2	295.2	295.2	227.4	199.2	198.2
	Result	NO.	1	2	m	4	S	9	7	80	6

26-DEC-2000; 2000WO-US35411.

WO200148164-A2 05-JUL-2001

Human genomic DNA Angiotensin conver Human ONEX ORF2025 Human NWDAR2 recep Human ONECHOLS Human ONECHOLS Human OSTEODIAST Congisporus Trypsi Human apoptosis pr Novel human apoptosis pr	Drosophila melanog Drosophila melanog Drosophila melanog Pseudorabies virus Human N-methyl-D-a Human N-methyl-D-a Human NMDARZC codi Human NMDA recepto Human NMDARZC codi Human NMDARZC codi Human NMDARZC codi Human N-methyl-D-a Human NMDARZC codi Human NMDARZC codi Human NMDARZC codi Human NMDARZC codi Human N-methyl-D-a Human N-methyl-D-a Human N-methyl-D-a Human N-methyl-D-a Human N-methyl-D-a	S ACVI) isoform #1	ing protein; beta-ASP; c receptor; beta-AR; sease; congestive heart failure; beta-ASP transgene; ss. cardiac ACVI isoform #1"231, aa:Xaa) n amino-acid; CDS does not
AAS11614 AAS06036 AAS06036 AAO79400 AAO79407 AAO79405 AAO79405 AAO79406 AAO79406 AAO79406 AAO79406 AAO79406 AAO79408 AAO80926 AAO80926 AAO80926 AAO80926 AAO80926 AAO80926	ABL17086 ABL17086 ABL19834 AAN 28210 AAN 28213 AAZ 38723 AAL 47372 AAN 82909 AAN 92909 AAN 92918 AAN 92918 AAN 92918 AAN 92918 AAN 92918	LIGNMEN	beta-adrenergic signalling protein therapy; beta-adrenergic receptor; adenylate cyclase; cAMP synthetase or kinase; GRK; heart disease; congclase VI; ACVI isoform; beta-ASP tricoation/Qualifiers 1.312 /*tag= a /*tag= a /*rag= a
	0.000000000000000000000000000000000000	314 7) enyle	lrener // bet it cy se; GR // Qual // Qual // Qual // Xaa i stop
236303 3050 3050 3050 3243 3243 4289 4325 4349 4349 4349 16046 668 1700 1700 1700	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	cDN	Human; cardiant; beta-adrenersite si myocardium; gene therapy; beta-adre adenylylcyclase; adenylate cyclase; G-protein receptor kinase; GRK; hea cardiac adenylcyclase VI; ACVI isof Homo sapiens. Location/Qualifiers Key Location/Qualifiers (*Fey Location/Qualifiers /*trag a n u include stop codon" /*EC_number= "4.6.1.
ruudadddddddo@@@r.		dard (fin	nnt; ise; se; cepto lcyc
		61 stan 61; -2001 partial	cardiant; lum; gene lcyclase; in recept adenylcy piens.
8 3 7 2 2 6 2 2 2 2 2 2 2 2 8 8 8 8 8 8 8 8 8		.08561 .08561; SEP-20	Human; cardiant; myocardium; gene adenylylcyclase; G-protein recept. cardiac adenylcy. Homo sapiens. Key CDS
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00 0000000000		RESULT AADO856 ID AA XX AC AA XX OV DT OV XX XX	KW KW KW KW KW KW KW KW KW KW KW
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                                                                                                                                                                      The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic signalling proteins (beta-ASP) which increase traceptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present CDNA sequence encodes human partial cardiac adenylcyclase VI (ACVI) isoform which is used for exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                   GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adenylylcyclase VI; AC-VI; beta-adrenergic signalling protein; transgene; gene therapy; congestive heart failure; cardiac function;
                                                                                                        Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
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                                                                                                                                                                                                                                                                                                                                                 Length 314;
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                                                                                                                                                    Example 5; Page 114; 153pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV23246 standard; cDNA; 2127
           99US-0472667
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                               (REGC ) UNIV CALIFORNIA
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                                                                          WPI; 2001-418260/44.
                                                    Gao M;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                       of the invention.
                                                                                    P-PSDB; AAE04308
          27-DEC-1999;
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                                                    Hammond HK,
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from the present invention. The present invention describes a recombinant replication-defective viral particle (I) comprising a gene encoding a beta-adranegic signalling protein (beta-ASP) operably inked to a promoter. Also described are: (I) a recombinant pro-viral plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably linked to a promoter and further comprising a replication-defective viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); an isolated polynucleotide comprising a sequence encoding a human adenyllycyclase isoform VI (AC-VI), or a variant having Ac activity; (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide comprising the polynucleotide of (3); (1) can be used to form a comprising the polynucleotide of (3). (I) can be used to form a cardiac function in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes human adenylylcyclase isoform VI (AC-VI)
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proteins – useful for gene therapy of congestive heart failure
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                                                                                                                                                             /product= "adenylylcyclase isoform VI"
/transl_except= (pos:229..231,aa:Xaa)
/transl_except= (pos:315..317,aa:Xaa)
/note= "no stop codon given; Xaa = unknown"
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/note= "n indicates a gap of about 0.5 kb"
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100.0%; Pred. No. 2.2e-69;
Live 0; Mismatches 0;
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Matches 314; Conservative
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adenovirus; ss
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                                                     Homo sapiens.
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/product= "Human cardiac adenylcyclase VI isoform #2"
/EC_number= "4.6.1.1"
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                                                                                                                                                                                                                                                                                                                  181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCANGCAAGGGCAAG
                                                              ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
                                                                                                      1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cardiant; beta-adrenergic signalling protein; beta-ASP; myocardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylaylcyclase; adenylate Gyclase; cAMP synthetase; G-protein receptor Kinase; GKK; heart disease; congestive hear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds
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  Pred. No. 7.1e-65;
); Mismatches 9;
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97.18;
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  Best Local Similarity 97.1
Matches 300; Conservative
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P-PSDB; AAE04311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cardiant; beta-adrenergic signalling protein; beta-ASP; mayocardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylate cyclase; cAMP synthetase; campate cyclase; cAMP synthetase; G-protein receptor kinase; GKK; heart disease; congestive heart failure; cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present DNA sequence encodes human cardiac adenylcyclase VI (ACVI) isoform which is used for generating a third beta-ASP transgene, used in the exemplification
                                         181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCANGCAAGGGCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Human cardiac adenylcyclase VI isoform #1"
/EC_number= "4.6.1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
                                                            Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                Human cardiac adenylcyclase VI (ACVI) isoform #1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 122-129; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                    AAD08563 standard; DNA; 3549
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                               301 GCGGGACCGCTGAA 314
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                                                                                                                         314
                                                                                                                         GCGGGACCGCTGAA
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Length 3549;

94.0%; Score 295.2;

Query Match

congestive heart failure;

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     to methods and compositions for enhancing
The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inscrting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian heart failure. The present DNR sequence encodes human cardiac adenylcyclase VI (ACVI) isoform which is used for generating a fourth beta-ASP transgene, used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                   121 CCCGGTATATGAGCTGCCTCCGGGATGCAGCCACCCAGCCCACCCCTGCGGGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                        CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGGGGCGCCCANGCAAGGGCAAG
                                                                                                                                                                                                                                                      1 AIGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
                                                                                                                                                                                                       DB 22; Length 3552;
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/product= "Human modified cardiac ACVI isoform"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human modified cardiac adenylcyclase VI (ACVI) isoform cDNA
                                                                                                                                                                                                    tch 94.0%; Score 295.2; DB 22; Length al Similarity 97.1%; Pred. No. 7.1e-65; 300; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                              Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
22..3525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD08568 standard; cDNA; 3582 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 GCCGGGACG 309
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                                                                                                                                                      of the invention.
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Synthetic.
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The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present colns sequence encodes human modified cardiac adenylcyclase VI (ACVI) isoform which is used for generating a beta-ASP transgene, used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 295.2; DB 22; Length 3582;
Pred. No. 7.1e-65;
0; Mismatches 9; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 143-150; 153pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.0%;
Best Local Similarity 97.1%;
Matches 300; Conservative
26-DEC-2000; 2000WO-US35411
                                                               99US-0472667
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                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                           WPI; 2001-418260/44
                                                                                                                                                                                              Hammond HK, Gao M;
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                                                               27-DEC-1999;
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being involved in the regulation of cardiac function and it is thought that decreased activity of adenylyl cyclase in the heart may be a major factor in the development of heart failure. Thus the adenylyl cyclase gene is useful to screen cpds. which stimulate the activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A canine heart cDNA library was constructed in lambda gt10 and was screened with a 970 bp AatI-HincII fragment from type I adenylyl cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl cyclase, which has significant homology to other previously known types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd. Positive colonies were subcloned into pUCIB and further subcloned and sequenced bidirectionally. The 5.4 kb clone was used to rescreen the library and on averlapping clone contg. the 5' end of the gene was isolated. Together the two clones cover the complete canine cardiac adenylyl cyclase gene. The gene is suspected of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purified DNA encoding cardiac adenylyl cyclase – useful to screen for cpds. which stimulate activity of the cyclase
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les 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Regulation; cardiac function; heart; heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 72.4%; Score 227.4; DB 14; Best Local Similarity 89.5%; Pred. No. 7.7e-48; Matches 256; Conservative 0; Mismatches 27; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
131..3627
/*tag= a
                                                                                                                                                                                                                                                AAQ42525 standard; DNA; 4046 BP.
                                                                                                                                                                                                                                                                                                                                                                                              Cardiac adenylyl cyclase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 2; 34pp; English
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                                                                                                                                                                                                                                                                                                                                              14-SEP-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-168873/21
                                                                                                                         445 GGCGGGACG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR37309
                                                                         301 GCGGGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-0CT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shikawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP543137-A
                                                                                                                                                                                                                                                                                                AAQ42525;
                                                                                                                                                                                                   RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW3059) that is expressed mainly in the heart and brain. AAC6 has a similar putative structure to other adenylyl cyclase isoforms but, like type V, is distinguishable in that it has a larger.

N-terminus and a relatively shorter C-terminus as it larges the C2b region. AAC6 CDNA was initially isolated from a human heart CDNA region. AAC6 CDNA was initially isolated from a human heart CDNA region. PAC6 CDNA was initially isolated from a human heart CDNA region. PAC6 CDNA was initially isolated from a human heart CDNA region. PAC6 CDNA sequence. The invention relates to the hAC6 compand to profited AAC6 and the full-length CDNA sequence. The invention relates to the hAC6 compand to profited AAC6 and the proteins made by these methods, antibodies against hAC6. Sene, methods for the recombinant production of purified AAC6 and the proteins made by these methods, antibodies against hAC6 correctors, probes and host cells (especially HEK-293) transformed by diagnostic and therapeutic uses for these various reagents. hAC6 can be used as a tool to screen for agonists and antagonists that in treating diseases caused by aberrant activity of this enzyme, and diseases whose symptoms can be ameliorated by stimulating or inhibiting the activity of hAC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGGCCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 CCCCGCTATATGAGCTGCCTCCGGGATGCAGACCACCCAGCCCCACCCCTGCGGGGCCCC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCANGCAAGGGCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence encodes human type VI adenylyl cyclase (hAC6, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newly isolated and purified human type VI adenylyl cyclase (hAC6) belypeptide - useful for identifying potential therapeutic agents that modulate hAC6 activity, and for the diagnosis of hAC6-associated diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGGAAAACAGCCTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 295.2; DB 20;
Pred. No. 7.5e-65;
0; Mismatches 9;
                                                                    Location/Qualifiers
145..3651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 1A-I; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            (CORT-) COR THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                     97US-0886550,
97US-0070904.
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ilarity 97.1%;
Conservative
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P-PSDB; AAW30599.
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Best Local Similarity
Matches 300; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomlinson JA;
                           Homo sapiens
                                                                                                                                                                    WO9901547-A1
                                                                                                                                                                                                                                                                       01-JUL-1998;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199102 to AB19912, encoding the protein sequences in ABB57020 to ABB5714) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                             180
                                                                                                              240
                                                                                                                               GACCAGTGGCTTCTGCACG 247
                                                                              307
                                        cccdectratrangagerbeceneedeatrecasecaeceaseceaeceaecee
                                                                ss.
                                                                                                            CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCCANGCAAGGGCAAG
which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                                                                                                                                                                                                                                                                                                                                             Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;
                                                                                                                                                                                              GAACTGGGGCTGCGGCCAGTGGCCCTGGGCTTCGAAGATACCGAAG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 1771-1780; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahashi Y,
                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                            ABI99680 standard; cDNA; 5841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _18-MAY-2001; 2001WO-JP04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-2000; 2000JP-0145977
                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-034733/04.
P-PSDB; ABB57257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200188188-A2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-2001
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                                                                          248
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A recombinant Adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzyme which allows easier screening of compounds that stimulate and inhibit adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimera of adenylyl cyclase C.l and C.2 domains linked covalently.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl cyclase, is activated by Gsalpha
              212
                                                                                                                                                      272
                                                                                                                                                                                                                    332
9
                                                                                         156 GAACGCAATGGGCAGAAGCG---CCCACGCCACGCGAATCGAGCCAGTGGCTTCTGCGCA
                                                                                                                                                                                                     GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG
                                                                                                                           121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC
                                                                                                                                                        213 CCTCGCTACATGAGCTGCCTCAAGAATGCGGAGCCACCCAGCCCCACTCCTGCAGCTCAC
 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
                                                                                                                                                                                     CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCANGCAAGGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyclic AMP; adenosine monophosphate; screening; stimulation; inhibition; treatment; Cholera; pituitary tumour; heart failure; ischaemia; endocrine disorder; cell necrosis; pseudohypoparathyroidism; endocrine deficiency; human; ss.
                                                                                                                                                                                                                                                                 133 GAGCTGGGGCTGCGGTCAGTGGCCTTGGGGTTTGACGACACTGAGGTGACCAC 385
                                                                                                                                                                                                                                                  241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAAC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenylyl cyclase; type I; type II; recombinant; enzyme; cAMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= Type VI adenylyl cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Type VI adenylyl cyclase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Columns 75-78; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
14..3556
                                                                                                                                                                                                                                                                                                                                                             BP,
                                                                                                                                                                                                                                                                                                                                                            AAA53923 standard; cDNA; 4131
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                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB02010.
                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-1995;
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DB 24; Length 5841;

Score 199.2; DB 24; Length Pred. No. 9.8e-41; 0; Mismatches 49; Indels

Query Match 63.4%; Best Local Similarity 82.3%; Matches 241; Conservative (

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	exon intron	exon		exon intron	exon	intron	FT exon 14876214883 FT /*tag= q FT //tumber= 10	exon	FT /*tag= s FT /number= 11 FT intron 150255153815 FT /*tag= t	/number= exon 153816		FT intron 154032158580 FT / tag= v / humber= 12 FT exon / tag= v / ftag=	intron	exon	F1 intron //thimber 14 FT intron //thimber 181006 FT /*tag= z	exon	intron	FT	/number= intron 183801
The domains may be linked by a linker peptide. The recombinant adenylyl cyclase is useful for screening inhibitors and stimulators of adenylyl cyclase activity. Inhibitors of the enzyme are useful for treating cholera, pituitary tumors, heart failure, ischaemia, cyclase are useful for treating pseudohypoparathyroidism and other cyclase are useful for treating pseudohypoparathyroidism and other xx sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;	Query Match 63.1%; Score 198.2; DB 21; Length 4131; Best Local Similarity 79.9%; Pred. No. 1.7e-40; Matches 246; Conservative 0; Mismatches 59; Indels 3; Gaps 1;	OY 1 ATGTCATGGTTTAGTGGCCTCCTGGTCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60	QY 61 GAACGCAATGGGCAGAAGCGTTCGGGCGCCGTGGCACTCGGCGCAGG 120	OY 121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGCCCACCCCAGCCCCTGCGGGCCCC 180	Qy 181 CCTCGGTGCCCCTGGCAGGAGGCCCTTCATCCGGAGGGCGAGGCCCANGCAAGGCCAAG 240 Db 233 ACTCGGTGCCCTTGGAGGTTCATCATCAGGAGGCTGGCCCGGGAAGGGTTG 292	Qy .241 GAACTGGGGCTGCGGGCACTGGGCTTCGAAGATACCGAAGTGACAACGA. 		RESULT 10	AMS.11014 y Standard; DNA; 236303 BP. XX AMS.11614 standard; DNA; 236303 BP. AC AMS.11614;		AXA BE Human genomic DNA containing exons 2-17 of the CRIM1 gene.	KW cRIM-1; Human; human chromosome 2p21-16.3; ophthalmological; KW neuroprotective; renal; osteopathic; dental; vulnerary; immunogen; KW antibody; gene therapy; neurodegenerative disease; eye disorder; cataract; bone morphogenic protein; BMG; renal disease; bone abnormality; KW tooth abnormality; wound; ds.	Homo s	AA Location/Qualifiers FT exon 3310433277	intron	exon	intron	FT /*tag= d //wmber=3 FT = xon 791047924	FT /*tag= e FT /number= 4

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The invention relates to nucleic acids from human chromosome 2p21-16.3
and the encoded peptide (and mouse and chicken orthologues) that
comprises a PGECCPLP group, an insulin-like growth factor binding protein
(IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group
and a transmembrane domain. The protein, e.g. CRIMI, interacts with
peptides of the transforming growth factor superfamily. A composition
comprising an expression construct comprising the nucleic acids of the
invention or a mimetic which antagonises or mimics an activity of a CRIMI
conprising any be used in a method for modulating the biological
activity of a polypeptide of the bone morphogenic protein (BMP) family.
In this way they may be used to prevent or treat an eye disease,
contracted formation. They may also be used to treat
contracted activity diseases, renal amange, e.g. by use of the nucleic acid in
abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in
activity contracted formation. They may also be used to treat
abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in
activity contracted products and skin damage, e.g. by use of the nucleic acid in
activity contracted against CRIMI polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 234445 CCCTACGCCGCAGCTCCTCCTCCTCCTCCTCCGCCGGACGCGGAAGTCCCCGCC 234386
                                                                                                                                                                                                                                                                                                                                                                                                                 peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 GCGTTCGCGCCCCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGGTATATGAGCTG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 CCTCCGGGATGCAGAGCCACCCAGCCCCTGCGGGCCCCCTCGGTGCCCCTGGCA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a Human genomic DNA containing exons 2-17 the CRIM1 gene.
                                                                                                                                                                                                                                                                                                                                Wilkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%; Score 39.8; DB 22; Length 236303; 55.4%; Pred. No. 1.8; 1.1ve 0; Mismatches 62; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids from human chromosome 2p21-16.3 and the encoded peuseful for preventing, diagnosing and treating e.g. eye disease, especially cataract formation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 236303 BP; 70199 A; 46544 C; 47996 G; 71563 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiotensin converting enzyme (ACEV) splice variant DNA #36.
                                                                                                                                                                                                                                                                                                                                Kolle G,
                                                                                                                                                                                                                                                                                                                                Georgas K,
              /number= 16
185153..187765
/*tag= ae
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                                                                                                                                                                                                                                                                                                                                Holmes G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 234385 TCTCGCCTCCTTCCTCCGG 234367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 3; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 GGATGACGCCTTCATCCGG 216
                                                                                                                                                                                                     24-NOV-2000;-2000WO-AU01435.
                                                                                                                                                                                                                                                99AU-0004348.
                                                                            /number= 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 55.4 les 77; Conservative
                                                                                                                                                                                                                                                                                      (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                Yamada T,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-343951/36.
                                                                                                                      WO200138519-A1
                                                                                                                                                                                                                                           26-NOV-1999;
                                                                                                                                                             31-MAY-2001.
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                                                                                                                                                                                                                                                                                                                              Little M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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AAS06036/c
                                          exon
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a DNA encoding an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the
              granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; ds; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 CAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 AGCTGCCTCCGGGATGCAGAGCCACCCACCCCACCCCTGCGGGCCCCCCTCGGTGCCCC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGTGAACGCAATGGG 72
Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis, renal diseases such as diabetic nephropathy, muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3050 BP; 520 A; 1032 C; 942 G; 555 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38.2;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 335-336; 519pp; English.
                                                                                                                                                                                  vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%;
                                                                                                                                                                                                                                                                                                                                           17-NOV-2000; 2000WO-IL00766.
                                                                                                                                                                                                                                                                                                                                                                                99IL-0132978.
99IL-0133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAU02936.
                                                                                                                                                                                                                                                          WO200136632-A2.
                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-1999;
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193 TGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCANGCAAGGCCAAGGAACTGGGGCTG 252

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Claim 11; Page 99-104; 156pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ79401;
                                                                                                                                                       Query Match
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                                                                                                                                                                                                                137
                                                                                                                                                                                     Matches
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   δλ
                                                                                                                                                                                                                                                                                                        요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antipsoriatic; antiparkinsoidan; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; antivitatic; antifungal; antirheumatic; antitifingmanatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis,
                                                                                                                                                                                                                                                                           cytostatic; hepatotropic; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                           Human ORFX ORF2925 polynucleotide sequence SEQ ID NO:5849.
                                                                       2383 CAGGCGGGCCGGTGCACCCAGCGGGCAGCGAGCTG 2348
                                                                                                                                                                                                                                                                           open reading frame; ORFX; detection;
                                                                                                                                                                                                                                                                                        vulnerary; antipsorlatic; antiparkinsonian;
                                              CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 5022-5024; 5507pp; English.
                                                                                                                                                  AAC77370 standard; cDNA; 3174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis; contraceptive; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0127607.
99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                             08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-602362/57.
P-PSDB; AAB43161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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05-APR-1999;
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                                                                                                                                                                                AAC77370;
                                              253
                                                                                                                       RESULT 12
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graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders; asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2109 AGGGCTTAGTCCAGTTCCTGGGGTGGGGGGCAGGCAGTGCCCTGGCACAGTGCCCAGGGT 2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2049 GCCCCCTCCAGGCTCAAGCTTCCAACCCACAGCCTCCGGGTCGCCACATTGCCCCTCAGC 2108
                                                                                                                                                                                                                                                                                                                                                                                                          GCCTCCGGGATGCAGACCAACCCAGCCCCACCCTGCGGGCCCCCCTCGGTGCCCTGGC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 AGGATGACGCCTTCATCCGGAGGGCGGCCCANGCAAGGGCAAGGAACTGGGGCTGCGGG 256
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of nucleic acids encoding related receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= part of the NMDAR2C receptor subunit 540..551
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/note= "24 bp insertion found in clone NMDA24"
                                                                                                                                                                                                                                                                                       DB 21; Length 3174;
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                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                              Sequence 3174 BP; 737 A; 897 C; 904 G; 620 T; 16 other;
                                                                                                                                                                                                                                                                                                                                              :69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NMDAR2 receptor subunit clone NMDA24 gene.
                                                                                                                                                                                                                                                                                                                      2.4;
                                                                                                                                                                                                                                                                                    Score 38.2; DB Pred. No. 2.4; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 CAGTGGCCCTGGGCTTCGAAGATACCGA 284
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1..822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "11 bp i
1501..1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ79401 standard; cDNA; 3243
                                                                                                                                                                                                                                                                                    12.2%;
ilarity 53.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0052449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-341863/42.
                                                                                                                                                                                                                                                                                                                Local Similarity
les 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR66059
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       The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)

receptor 2C (NMDAR2C) gene clone NMDA24. This clone covers bases

861-4068 of the complete NMDAR2C gene (AAQ79372) with an insertion of 11

bp between bases 1300-1 and an insertion of 24 bp between bases 2350-1.

The 11 bp insert adds an extra 3 a. to the peptide sequence but causes

a reading frame shift which terminates the peptide at residue 494 of the

NMDAR2C sequence. The NMDA receptor contains two subunits R1

(AAQ79370) and subunit R2 selected from the subunits 2A (AAQ79375), 2B

(AAQ79377), 2C and 2D (AAQ79378). The receptor forms part of a family of

NMDA receptors which have cation-selective channels and bind quitamate

and NMDA. The NMDAR2C gene was obtained by amplifying cDNA derived from

human brain tissues with primers corresponding to sequences in the rat

NMDAR2A receptor DNA and using the resultant fragments as probes to

screen a cDNA library derived from human hippocampal RNA. 4 basic clones

were isolated: NMDA21 (AAQ79399), NMDA22 (AAQ79400), NMDA24 (AAQ79401)

and NMDA26 (AAQ79402). The clones are thought to be splice variants of

each other. Based on the sequence of the 4 clones, a series of variants

(AAQ79403-7) of the NMDAR2C receptor were constructed. The expression of

the genes allows the reconstruction of the NMDA receptor. The complete

receptor can be used to identify compounds which bind or are antagonistic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2926 AGAGGCCCCCAGGCCCCGGAGAGCCAGGAGCCGTGGCACAGGGTGGAAGGTGAAGGA 2867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 CAGAAGCGTTCGCGGCGCCCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AGCIGCCICCGGGAIGCAGAGCCACCCAGCCCACCCTGCGGGCCCCCCTCGGTGCCCC 192
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           13 AGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGTGAACGCAATGGG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2806 recreccadecededececeracerecerecerecereseasecrecegardarese
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                                                                                                                                                                                                                                                                                                                                                                 Length 3243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "11 bp insertion found in this clone"
1604..1605
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                      Sequence 3243 BP; 540 A; 1115 C; 1024 G; 564 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                12.2%; Score 38.2; DB 15;
46.0%; Pred. No. 2.5;
tive 0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= NMDA22 variant NMDAR2C
1034..1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2686 cacececececrecaccasces de casecas 2651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor subunit clone NMDA22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 3..1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ79400 standard; cDNA; 3698
                                                                                                                                                                                                                                                                                                            to the human NMDA receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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AAQ79400/c
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The including sequence of the movel of the coperate (NMDARZC) gene clone (AAQ/9372) with an insertion of 11 pp between bases 1300-1 and a 15 bp deletion of bases 1960-74. The 11 bp insert adds an extra 3 a.a. to the peptide at residue 494 of the NWDARZC frame shift which terminates the peptide at residue 494 of the NWDARZC sequence. The NWDA receptor contains two subunits: subunit R1 (AAQ/9370) and subunit R2 selected from the subunits 2A (AAQ/9375), 2B (AAQ/9377), 2 c and 2D (AAQ/9378). The receptor forms part of a family of NWDA receptors which have cation selective channels and bind glutamate and NWDA. The NWDARZC gene was obtained by amplifying cDNA derived from human brain tissues with primers corresponding to sequences in the rat NWDARZA receptor DNA and using the resultant fragments as probes to soreen a cDNA library derived from human hippocampal RNA. 4 basic clones were isolated: NWDA21 (AAQ/9399), NWDA22 (AAQ/9400), NWDA24 (AAQ/9401) and NWDA26 (AAQ/9402). The clones are thought to be splice variants of each other. Based on the sequence of the 4 clones, a series of variants (AAQ/9403-7) of the NWDARZC receptor where constructed The expression of the burnar when we have constructed are expression of the burnar when we have constructed the expression of the burnar when we have a complete the technique of the NWDA receptor. The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3321 CAGACAGCCCCCCAGCAAAATGGCAGGTGGGCGTGGCGGCGTGCAGACGTGCTG 3262
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/*tag= c
/note= "15 bp deletion of NWDAR2C sequence between
these bases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of nucleic acids encoding related receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liaw CW,
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us-09-750-240-1.rng

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The nucleotide sequence of the novel N-methyl-D-aspartate (NWDA)
receptor 2C (NWDAR2C) gene clone NWDAR2C-delta15-delta51. This clone
contains bases 1-1959, 1975-2350 and 2402-4068 of the complete NWDAR2C
sequence (AAQ79372). The variant differsifrom the full length sequence by
a 15 bp deletion of bases 1960-74 and a 51 bp deletion of bases
2351-2401. A series of variants (AAQ79403-7) of the NWDAR2C receptor
were constructed, by recombination, based on the sequence of the 4 basic
clones: NWDA21 (AAQ79399), NWDA22 (AAQ79400), NWDA24 (AAQ79401) and
NWDA2 (AAQ79370) and subunit R2 selected from the subunits 2A (AAQ79375), 2B
(AAQ79377), 2C and 2D (AAQ79378). The receptor forms part of a family of
NWDA receptors which have cation-selective channels and bind glutamate
and NWDA receptor. The complete receptor can be used to identify compounds
which bind or are antagonistic to the human NWDA receptor.
                                                                                                                                                      N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNAl; NMDA receptor; antagonist; ds.
                                                                                                                                                                                                                                               /*tag= a
/product= NMDAR2C-delta15-delta51 receptor subunit
1959..1960
                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
/note= "51 bp deletion of NMDAR2C sequence between
these bases"
                                                                                                                                                                                                                                                                                                                          /note= "15 bp deletion of NMDAR2C sequence between these bases"
                                                                                                                         Human NMDAR2 receptor subunit clone NMDAR2C-delta15-delta51 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of nucleic acids encoding related receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4274 BP; 713 A; 1462 C; 1331 G; 768 T; 0 other;
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                                                                                                                                                                                                                                  Location/Qualifiers
189..3833
                             AAQ79407 standard; cDNA; 4274 BP.
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P-PSDB; AAR66065.
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                                                           AAQ79407;
RESULT 15
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                AAQ79407,
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3685 AGAGGCCCCCAGGAGAGCCAGGAGAGCCGTGGCTGGCACAGGGTGAAGGTGAGGA 3626
                                                                                               73 CAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGTGGCTTCTGCACGCCCCCGCTATATG 132
                                                                                                                                 133 AGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCAGCCCTGCGGGCCCCCTCGGTGCCCC 192
                                                                                                                                                                                                                 193 TGGCAGGATGACGCCTTCATCCGGAGGGCGGCCCANGCAAGGCCAAGGAACTGGGGCTG 252
                                                                                                                                                                                                                                                                                                                              253 CGGCCAGTGCCCTGGGCTTCGAAGATACCGAAGTG 288
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12.2%; Score 38.2; DB 15; Length 4274;
Best Local Similarity 46.0%; Pred. No. 2.6;
Matches 127; Conservative 0; Mismatches 149; Indels 0;
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February 28, 2003, 21:13:01; Search time 539.139 Seconds (without alignments) 16949.756 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

em_htgo_hum:* em_htgo_mus:*

em_htg_mam:* em_htg_vrt:*

PAT 17-DEC-2001

linear

DNA

AR174471 314 bp 326uence 1 from patent US 6306830. AR174471 GI:17914791

RESULT 1
AR174471
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

Tobases 1 to 314)
Hammond, H.Kirk., Insel, P.A., Ping, P., Post, S.R. and Gao, M. Gene therapy for congestive heart failure
Patent: US 5306830-A 1 23-OCT-2001;
Location/Qualifiers

REFERENCE AUTHORS TITLE JOURNAL FEATURES

Unclassified.

Unknown. Unknown.

SOURCE ORGANISM

AB007882 Homo sapi AC117498 Homo sapi AC021647 Homo sapi AC02557 Homo sapi AC02557 Homo sapi M9468 Canis famil 129958 Sequence M93422 Mouse adeny AC074028 Muss muscu AR106659 Sequence M96160 Rattus norv AC1115 Rattus norv AC12405 Rattus no AC056835 Rattus no M96653 Mus musculu U72404 Fugu rubrip AF429315 Homo sapi L14320 Bovine herp AY016020 Gallus ga AJ004801 Bovine he AJ004801 Bovine he AL096852 Streptomy AC120284 Rattus no AC113912 Rattus no AC040912 Homo sapi AC110369 Rattus no AC118939 Rattus no AC128294 Rattus no AC120273 Rattus no AC120273 Rattus no Oryza sat Rattus no Rattus no Rattus no Homo sapi Rattus no Mus muscu Sequence Sequence Sequence AX189757 Sequence Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AC100791 F AC128569 F AC068500 N AL096852 S AX189768 ALIGNMENTS SUMMARIES MUSADNLCYC AX189761 AX189766 AX189766 AX007882 AC117498 AC021647 AF250226 AC025557 DOGADENCYC AC074028 AR106659 RATADCYB AX305965 MUSADCYC BHV1CGEN BHV1CGEN RATADC AC129405 AC096835 AF429315 AC011995 AC102955 AC096161 AC127964 AC100791 AC128569 AC120284 AC113912 AC040912 AC110369 AC118993 AC128294 AC119440 AY016020 AC120273 072484 200 100 10 DB 94.0 94.0 94.0 94.0 94.0 94.0 94.0 93.5 94.0 93.5 93.0 93.0 93.0 93.0 93.0 93.0 93.0 93.0 94.0 93.0 94.0 93.0 93.0 94.0 93.0 94.0 93.0 94.0 93.0 94.0 93.0 94.0 93.0 94.0 93.0 94.0 Length Query 40.8 40.8 40.6 40.4 293.6 292 196.6 186.2 43.4 Score 41.8 Result Š. υo U U O υO 0000

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Hammond, H.K. and Gao, M.
Hammond, H.K. and Gao, M.
Gene therapy for congestive heart failure
Patent: WO 0148164-A 1 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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Pred. No. 7.3e-60;
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                                           Query Match 99.7%; Score 313; DE Best Local Similarity 100.0%; Pred. No. 7.3 Matches 314; Conservative 0; Mismatches
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Sequence 1 from Patent W00148164.
AX189757
AX189757.1 GI:15143133
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98 c 108 g
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AX189757
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4.8e-56;
0; Mismatches 9;
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Hammond, H.Kirk., Insel, P.A., Ping, P., Post
Gene therapy for congestive heart failure
Patent: US 6306330-A 5 23-OCT-2001;
Location/Qualifiers
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Sequence 5 from patent US 6306830.
AR17473 GI:17914793
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Sequence 5 from Patent WO0148164.
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Best Local Similarity 97.1%;
Matches 300; Conservative
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synthetic construct
artificial sequences.
1 (bases 1 to 3582)
Hammond, H.K. and Gao, M.
Gene therapy for congestive heart failure
artent: WO 0148164-A 12 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
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/organism="synthetic or/db_xref="taxon:32630"
/note="Modified_AC-VI"
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Hammond, H.K. and Gao, M.
Gene therapy for congestive heart failure
Patent: WO 0148164-A 10 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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1 (bases 1 to 3549)

Hammond, H.K. and Gao, M.
Gene therapy for congestive heart failure
Patent: WO 0148164-A 5 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
Location/Qualifiers
                                                                                                                                                        Score 295.2; DB 6;
Pred. No. 4.8e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 from Patent W00148164.
                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
1025 c 1061 g 76
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/db_xref="taxon:9606"
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97.1%;
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Matches 300; Conservative
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/clone_lib="pBluescriptII SK plus"
/note="This sequence was obtained by subcloning of the DNA
fragments derived from two cDNA clones (1 - 1352 was
derived from pg00161 and 1353 - 5877 was derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-00T-1997) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarau, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, On May 9, 2002 this sequence version replaced gi:2887418.
Sequence updated (05-Jan-1998).
Location/Qualifiers
1...5877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="GRRTAGGTARTRGLGGPRDGRPAGRSPRGRRGGGPGQARSRAGS NMSWFSGLLVPRVDERKTAWGERNGQKRSRRRGTRAGGFCTPRYMSCLRDAEPPSPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMLGIYASIFLLLITYLICAVYSCGSLFPKALQRLSRSIVRSRAHSTAVGIFSVLLV
FTSAIANMYFIGNMLLSLLASSVFLHISSIGKLAMIFVLGLIYLVLLLLGPPATIFDN
                      PRI 10-MAY-2002
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DFLWKLQATGEKEEMEELQAYNRRLLHNILPKDVAAHFLARERRNDELYYQSCECVAV
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AASGLNASTYDQVGRSHITALADYAMRLMEQMKHINEHSFNNFQMKIGLNMGPVVAGV
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                                                                                                                                                                                                                              Ishikawa,K., Nagase,T., Nakajima,D., Seki,N., Ohira,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain which code for large proteins in vitro
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:hh01205s1.
                        linear
            Homo sapiens KIAA0422 mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hh01205s1"
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/gene="KIAA0422"
<1. .3484
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/codon_start=2
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                                                                              AB007882.2 GI:20521044
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94.0%; Score 295.2; DB 9; Length 5877;

Query Match

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Home sapiens appears the control of 
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Homo sapiens clone RP11-422021, *** SEQUENCING IN PROGRESS ***, 20
unordered pieces.
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Pred. No. 4.4e-56;
0; Mismatches 9;
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HTG; HTGS_PHASE1.
Best Local Similarity 97.1
Matches 300; Conservative
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NOTE: This is a "vorking draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                 Direct Submission
Submitted (10-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 Chases 1 to 205248)
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, Taylor, T., Tayloro, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                           Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 29, 2002 this sequence version replaced g1:21956504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: WUGSC
Contact: hgsc-help@bcm.tmc.edu
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31033:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16697
                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                        Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2026
2126
4438
4538
6634
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25346
25446
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31134
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AUTHORS
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JOURNAL
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ACO21647 193283 bp DNA linear HTG 09-MAY-2002
Homo sapiens chromosome 12 clone RP11-455122, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168999 CCCCGCTATATGAGCTGCCTCCGGGATGCAGCCACCCAGCCCCACCCTGCGGGCCCC 168940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168939 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCCCAGGCAAGGGCAAG 168880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 168879 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACGCG 168820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases, 1 to 193283)

Muzny, D.M. Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chowdhry, I., Christopoulos, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 169059 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 169000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCCANGCAAGGGCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCCAGCCCCAGCCCTGCGGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 295.2; DB 2; Length 205248; Pred. No. 2.6e-56;
35963: gap of unknown length 49814: contig of 13851 bp in length 49814: gap of unknown length 64885: contig of 14471 bp in 64485: gap of unknown length 81100: contig of 16615 bp in length 81200: gap of unknown length 97966: contig of 16766 bp in length 98066: gap of unknown length 115533: gap of unknown length 115633: gap of unknown length 139873: contig of 24240 bp in length 139873: gap of unknown length 139873: gap of unknown length 17564: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6006 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .205248
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-42202]
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97.1%;
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delaney, K.R., Delaney, K.J., Delaney, K.J., Delaney, K.J., Delaney, K.J., Delaney, K.J., Douthwaite, K.J., Delaney, R.J., Durbin, K.J., Douthwaite, K.J., Darper, H., Doyan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Elagg, M., Ford, J., Eoster, P., Frantz, P., Garlsi, A., Garca, M., Gill, R., Gao, J., Garca, W., Garner, T., Garza, N., Gill, R., Gorell, J.H., Guevara, W., Garner, T., Hawes, A., Hamandez, O., Hodgson, A., Hogues, M., Holloway, C., Hallins, B., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolives, S., June, J., Kovar, C., Karloson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Lude, C., Lidu, J., Liu, W., Loulseged, H., Lozacoo, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Lu, J., Lu, X., Lucier, A., Lucier, R., Luna, R., Marinez, E., Mahesbwari, M., Matchal, F., Morden, M., Matchal, F., Morgen, M., Matchal, F., Morgen, M., Matchal, F., Morgen, M., Mutchel, F., Mutc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: RP11-455122

Center clone name: RP11-455122

Center clone name: RP11-455122

Sequencing vector: Plasmid;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: Phrag; version 0.990329
Consensus quality: 219180 bases at least Q40
Consensus quality: 233400 bases at least Q30
Consensus quality: 23367 bases at least Q20
Estimated insert size: 209025; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morley, KfC.

Direct Submission
Submitted (19-7AN-2000) Human Genome Sequencing Center, Department of Molecular and Human Generics, Baylor College of Medicine, One Baylor Plazar—Houston, TX 77030, USA
3 (bases 1 to 193283)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 to 193283
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AUTHORS
TITLE
JOURNAL
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JOURNAL
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COMMENT

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PRI 15-SEP-2000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 6463)
Wicker,R., Catalan,A.G., Cailleux,A., Starenki,D., Stengel,D.,
Sarasin,A. and Suarez,H.G.
Cloning and expression of human adenylyl cyclase type VI in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GAACGCAAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCCAGCCCCCACCCCTGCGGGCCCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCCANGCAAGGCCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAAACGACACCCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens adenylyl cyclase type VI mRNA, complete cds. AF250226.1 GI:9049782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 193283;
                                                                                          2133: contig of 2133 bp in length 2233: gap of unknown length 5400: contig of 3167 bp in length 5800: gap of unknown length 7889: contig of 2389 bp in length 7889: contig of 2389 bp in length 35756: gap of unknown length 65517: contig of 23661 bp in length 65717: gap of unknown length 65717: gap of unknown length 65717: gap of unknown length 65718: gap of unknown length 104448: contig of 38731 bp in length 104548: gap of unknown length
                                                                                                                                                                                                                                                                                                                      145966: contig of 41418 bp in length
146066: gap of unknown length
193283: contig of 47217 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.5%; Score 293.6; DB 2; 96.8%; Pred. No. 6.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49273 a 48888 c 46863 g 47544 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP11-455122"
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74471 GGCGGGACG 74463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                 2234
5401
5401
7890
7990
35657
35757
65618
65718
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145967
146067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      source
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AF250226
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACGACCACG 300
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1962: gap of unknown length
3736: contig of 1774 bp in length
3836: gap of unknown length
6925: contig of 3089 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
length
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bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of unknown 1. contig of 4748 bg egap of unknown 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates;
1 (bases 1 to 171945)
Waterston, R.H.
                                                                                                                                                                                                                                                                                           AC025557.4 GI:7657832
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 171945)
Waterston R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6925:
7025:
11773:
11873:
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19505:
26329:
26429:
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                  995 GGCGGGACG 1003
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                            301 GCGGGACCG 309
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SCLRDAEPPSPPROPWODDAFIRRGGPGKGKELGLRAVALGFEDTEVTTAGG
TAEVAPDAVPRSGRSCWRRLVQVPGSKGFRSAKLERLYCORFPGWNGSSELTLANTLY
LLTAVLLAFHAAPARROGPAVALLACAAALFVGRAVVORFSRGDSWAVVSYVVUGI
LAAVQVGGALAADPRSPSAGLMCQPVFTVYIAYLLPIRMRAVLSGLGLSTLHLILAW
QLNRGDAFUWKOLGANVLLEPCTNVTGICTHYPAEVSGRAFORFSRGYIGARLHLOHE
NRQOGRILLSVLPQHVAMERKEDINTKKEDWMFHKIYIGKHDVVSILFADIEGFTSLA
SQCTAQELVWTLNELPARFDKLAAENHCLRIKILGOCYTCVSGLDEARADHAHCCVEM
GYDMIEAISLVREVTGVNVMRVGTHSGRVHGCVLGLRKWQFDVWSNDVTLANHHREAG
GRAGRIHTRATLQYLNGDYEVPEFRGGERNAYLKEQHIEFTLILGASQKRKEEKAML
AKLORTRANSMEGLAMPRWPDRAFSRTKDSKAFROMTDDSSKDNRGTQDALNPEDEV
DDFLERRAIDARSIDQLRKUHPERFLIFFQREDLEKKYSKRVDPRFGAYVACALLYFCF
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HSTAVGIFSVLLVFTSAIANMFTCNHTPIRSCAARMLNLTPADITACHLQQLNYSLGL
DAPLCEGTMPTCSFPEYFIGNMLLSLLASSVFLHISSIGKLAMIFVLGLIYLVLLLLG
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OVESTARLDFLWKLQATGEKEEMEELQAYNRRLLHNILPKDVAAHFLARERRNDELYY
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KTIGSTYMAASGLNASTYDQVGRSHITALADYAMRLMEQMKHINEHSFNNFQMKIGLN
MGPVVAGVIGARKPQYDIWGNTVNVSSRMDSTGVPDRIQVTTDLYQVLAAKGYQLECR
                                                                                                                                                                  genetique et cencer UPR 2169, Institut de Recherches sur le Cancer CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France Location/Qualifiers
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                                                                                                                                Direct Suprission Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
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Wicker, R., Gascon Catalan, A., Cailleux, A.-F., Starenki, D.,
Stengel, D., Sarssin, A. and Suarez, H.G.
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                Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000) 20435313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="adenylyl cyclase type VI"
/protein_id="AAF82478.1"
/db_xref="GI:9049783"
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96.4%; Pred. No. 2.3e-55;
iive 0; Mismatches 11
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                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                             /tissue_type="thyroid"
complement(19. .447)
/rpt_family="Alu"
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469. .561
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695. .4201
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/rpt_family="MIR"
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AC025557 17945 bp DNA linear HTG 07-JUL-2000 Homo sapiens chromosome 12 clone RP11-579D7, WORKING DRAFT SEQUENCE, 17 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Direct Submission
Submitted (10-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Mn 03198, IISA
On Apr 27, 2000 this sequence version replaced gi:7574970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; 100%
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 167959 bases at least 030
Consenus quality: 168924 bases at least 020
Insert size: 177000; agarose-fp
Insert size: 177005; sum-of-contigs
Quality coverage: 5.62 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
Center code: WUGSC
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DOGADENCYC 4046 bp mRNA linear MAM 27-APR-1993 Canis familiaris adenylyl cyclase type VI mRNA sequence.
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1 (bases 1 to 4046)

Ratsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Halnon,N.J., Homcy,C.J. and Ishikawa,Y.

Cloning and characterization of a sixth adenyly—eyelage isoform: types V and VI constitute a subgroup within the marmerian adenyly)
                                                                                                                   CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
                                                                                                                                                                                                                    241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACG 300
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92409599
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adenylyl cyclase type VI.
canis familiaris cardiac muscle cDNA to mRNA.
Canis familiaris
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1. .4046
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/tissue_type="cardiac muscle"
a 1206 c 1254 g 843 t
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ilarity 89.5%;
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DOGADENCYC
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                                                                                                                                                                      97622: gap of unknown length 110884: contig of 13262 bp in length 110984: gap of unknown length 126977: contig of 15993 bp in length 127077: gap of unknown length 146137: contig of 19060 bp in length 146137: contig of unknown length 14627: contig of 19060 bp in length 171945: contig of 25708 bc. i.
                                                                      f unknown length
o of 9898 bp in length
f unknown length
o f 9920 bp in length
f unknown length
o of 12235 bp in length
f unknown length
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Pred. No. 1.3e-53;
0; Mismatches 9; Indels
                                                        of 10142 bp in length
of 7165 bp in length
unknown length
of 8454 bp in length
                                            unknown length
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110985. .126977
/note="assembly_name:Contig19"
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146238. 171949.
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/note="assembly_name:Contig9"
19506. .26229
/note="assembly_name:Contig10"
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33695. .42148
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7026. .11773
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3837. .6925
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/chromosome="12"
                                                                                                                                                                                                                                                                                                       Cocation/Qualifiers
              gap of contig gap of contig
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gap of
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1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60

241 GAACTGGGGCTGCGGCCAGTGGCCCTGGGCTTCGAAGATACCGAAG 286

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/translation="MSWFSGLLVPKVDERKTAWGERNGGKRPRHANRASGFCAPRYMS
CLRNBEPSPEPPAHTRCPWQDEAFIRRAGPGSVBCLGLRSVALGFDDTSTTPWGTA
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MAVLLTFHAAPAQPQPAYVALLTCASVLFVVLMVVCNRHSFRQDSMWVVSYVVLGILA
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STARLDFLWKLQATGEKEEMEELQAYNRRLLHNILPKDVAAHFLARERRNDELYYQSC
ECVAVWFASIANFSEFYVELEANNEGVECLRLLNEIIADFDEIISEERFRQLEKIKTI
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VVAGVIGARKPQYDIWGNTVNVSSRMDSTGVPDRIQVTTDLYQVLAAKGYQLECRGVV
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Yoshimura, M. and Cooper, D. M. Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase from NCB-20 cells
Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
92357702
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                                                                  61 GAACGCAAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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                     Gaps
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                                                   1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
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                    Indels
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/protein_id="AAA37174.1"
/db_xref="GI:191691"
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adenylyl cyclase; adenylyl cyclase type VI.
Mus musculus cDNA to mRNA.
Pred. No. 1.1e-34;
                    0; Mismatches
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/db_xref="taxon:10090"
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1. .5841
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96. .3593
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   82.3%;
                    241; Conservative
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Matches 241; Conserv
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Lahkawan dawa da characterization of a cardiac adenylyl cyclase
Patent: US 5578481-A 1 26-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y. Method for examining ischemic conditions
Patent: WO 0188188-A 716 22-NOV-2001;
School Juridical Person Nihon University (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                          Length 4046;
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Pred. No. 6.2e-41;
0; Mismatches 27
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Sequence 716 from Patent WO0188188.
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                                                                                             A046 bp Sequence 1 from patent US 5578481
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                              Query Match 63.4%; Score 199.2; DB 10; Length 5841; Best Local Similarity 82.3%; Pred. No. 1.1e-34; Matches 241; Conservative 0; Mismatches 49; Indels 3;
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Result

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APPLICANT: Hammond, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Ding, Peipei
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
          US-08-480-474-53

US-08-940-086A-53

US-08-940-086A-53

US-08-935-105A-53

US-09-648-273A-49

US-08-231-193A-49

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US-08-940-035A-49

US-08-931-193A-47

US-08-231-193A-47

US-08-231-193A-47

US-08-480-474-47

US-08-480-474-47

US-08-480-477-49
                                                                                                                                                                                                                    US-08-940-035A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/008,097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22000-20567.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFRAX: 650-494-0792
                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09008097 Patent No. 6306830 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence LOCATION: 1...312 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTAL. ....
ZIP: 94304-1018
COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
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nucleic acid
NDEDNESS: double
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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Sequence 5, Appli
Sequence 44, Appli
Sequence 44, Appl
Sequence 43, Appl
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Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 1, Appli
                                                                                                   (without alignments)
12520.796 Million cell updates/sec
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                                                                                     February 28, 2003, 22:03:11; Search time 7.69093 Seconds
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Seguence 5,
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-940-035A-43
US-08-935-105A-43
US-09-648-797-43
US-08-231-193A-53
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US-08-910-035A-44
US-08-910-035A-44
US-08-910-035A-44
US-08-910-035A-44
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US-09-474-076-1
US-08-726-214-11
US-08-726-214-11
US-09-404-650-12
US-07-793-961A-1
US-08-240-351-1
US-08-28-069-5
US-08-928-069-5
US-08-928-069-5
                                                                                                                                                                                                                                                      Potal number of hits satisfying chosen parameters:
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US-08-486-273A-43
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                                                                                                                                                                                                                               441362 segs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             using sw model
                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                        US-09-750-240-1
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Gaps

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Length 3549; Indels 9

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APPLICANT: TONLINSON, James E.
APPLICANT: CON Therapeutics, Inc.
TITLE OF INVENTION: CLOUNING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5028-01-US
CURRENT APPLICATION NUMBER: US/09/474,076
CURRENT FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: PCT/US98/13694
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1997-07-01
SPRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
SPRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                       61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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les 9;
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Pred. No. 3.5e-66;
0; Mismatches 9;
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Pred. No. 3.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: human type VI adenylyl cyclase
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; Patent No. 6465237
; GENERAL INFORMATION:
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                                                                                           ; NAME/KEY: Coding Sequence; LOCATION: 1...3501
; OTHER INFORMATION:
US-09-008-097-5
                                                                                                                                                                                               Query Match 94.0%;
Best Local Similarity 97.1%;
Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.0
Best Local Similarity 97.1
Matches 300; Conservative
                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-09-474-076-1
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Best Local Similarity
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LENGTH: 49
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                                                                                                                                    Gaps
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                                      Length 314;
                                                                             Indels
                                    99.7%; Score 313; DB 4; I
100.0%; Pred. No. 7.1e-71;
Live 0; Mismatches 0;
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APPLICANT: Insel, Paul A.
APPLICANT: Ping, Peipei
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-008-097-5; Sequence 5, Application US/09008097; Patent No. 6306830; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dylan, Tyler M
REGISTRATION UNDBER: 2200
REFERENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:
TELEFRANE 650-813-5600
TELEFRAN: 706141
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                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GCGGGACCGCTGAA 314
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CORRESPONDENCE ADDRESS:
                                      Query Match
Best Local Similarity
Matches 314; Conserv
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
US-09-008-097-1
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Gaps 1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAAACAGCCTGGGGT 60 ö Indels

us-09-750-240-1.rni

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191 GAACGCAATGGGCAGAAGCGT---CCACGCCGCGGACCTGGACCAGTGGCTTCTGCACG 247
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                                                                                                                                                                                                248 CCCCGCTATATGAGCTGCCTCCGGGATGCGCACCCCCCAGTCCCACCCCTGCGGGCTCCC 307
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 Gaps
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 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08240357
Patent No. 5578481
GENERAL INFORMATION:
APPLICANT: ISHIKAWA YOSHIHITO
TITLE OF INVENTION: Cloning and Characterization of a TITLE OF INVENTION: Cardiac Adenylyl Cyclase NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 227.4; DB 1;
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 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gordon, Alan M.
REGIZTRATION UNUBER: 30,637
REFERENCE/DOCKET NUMBER: 31,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One Cyanamid Plaza
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4046 base pairs
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 Matches 256; Conservative
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COMPUTER READABLE FORM:
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Best Local Similarity
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MOLECULE TYPE:
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LOCATION:
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                                                                                                                        121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCC 180
                                                                                                                                             265 CCCGGTATATGAGCTGCCTCCGGGATGCAGACCACCCAGCCCCACCCCTGCGGGGCCCC 324
                                                                                                                                                                                                CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCANGCAAGGCCAAG 240
                                                                                                                                                                                                                   145 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAATGGAAAAAAGGCCTGGGGT 204
                                                                                                                                                                                                                                                                       GAACTGGGGGTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACGACGACG 300
                                                     GAACGCAATGGGCAGAAGCGTTCGCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPLICANT: Yoshihiro Ishikawa
TITLE OF INVENTION: Cloning and Character-
TITLE OF INVENTION: Lization of a Cardiac Adenylyl Cyclase;
NUMBER OF SEQUENCES: 1
CORRESPONDENCES: Alan M. Gordon
ADDRESSEE: Alan M. Gordon
ADDRESSEE: Alan M. Gordon
STREET: 1937 West Main Street,
STREET: P0.0. Box 60
CITY: Stamford
STATE: Connection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4046;
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Pred. No. 4.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC ... COMPUTER: OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII from DW4 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/793,961A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31,705
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203 321 2719
TELEFAX: 203 321 2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07793961A
Patent No. 534521
GENERAL INFORMATION:
APPLICANT: YOShihiro Ishikawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.48;
89.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS LENGTH: 4046 base pai. TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19911118
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Connecticut: USA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-793-961A-1
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                                                                                                                                                                                                                                                                       241
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GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
APPLICANT: Dietrich, Paul S.
APPLICANT: MGIVENTION: J-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT APPLICATION NUMBER: US/09/404,650
SOFTWARE: PALENCE: L199-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 12
LENGTH: 6503
                                                                                                                                                                                                 233 ACTCGGTGCCCCTGGCAGGATGAAGCCTTCATCAGGAGGGCTGGCCCGGGAAGGGGTGTG 292
                                          CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGGCCCC 180
    116 GAACGCAATGGACAGAAGCG---CCCACGCCAGGCGACCCGAGCCCGTGGCTTCTGCGCG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 CCGGGATGCAGACCACCCAGCCCCACCCTGCGGGCCCCCTCGGTGCCCCTGGCAGGA 200
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                                                               CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGGCGCCCCANGCAAGGCCAAG
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APPLICANT: Yoshihiro Ishikawa
TITLE OF INVENTION: 1zation of a Cardiac Adenylyl Cyclase
TITLE OF INVENTION: 1zation of a Cardiac Adenylyl Cyclase
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Alan M. Gordon
ADDRESSE: American Cyanamid Company
STREET: 1937 West Main Street,
STREET: Lo. Box 60
CITY: Stanford
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6503;
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                                                                                                                                                                                                                                                                                                                                                                                            US-09-404-650-12/c
; Sequence 12, Application US/09404650
; Patent No. 6309858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/07793961A Patent No. 5334521
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55.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Rattus sp.
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Best Local Similarity
                                                                                                                                                                                                                                                                              GCGGGACC 308
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US-07-793-961A-1/c
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131 ATGTCGTGGTTTAGTGGCCTCCTGGTCCCCAAAGTGGATGAACGGAAGACAGCCTGGGGT 190
                                      GAACGCAATGGGCAGAAGCGTTCGCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
                                                        248 CCCGGCTATATGAGCTGCCTCCGGGATGCGCACCCCCCAGTCCCACCCCTGCGGGCTCCC 307
                                                                                                                                                                                                   240
                                                                                                                                                                                                                   GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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                                                                                                                 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCC
                                                                                                                                                                                               CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCANGCAAGGGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Tang, Wei-Jen
APPLICANT: Gliman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SECUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            241 GAACTGGGGCTGCGGCCAGTGGCCCTGGGCTTCGAAGATACCGAAG 286
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTAME: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: U$/08/726,214

FILING DATE: CONCULTENTLY HENWITH

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: U$ 60/005,498

FILING DATE: 04-0CT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REFERENCE/DOCKET NUMBER: J7,642

REFERENCE/DOCKET NUMBER: J7,642

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEPHONE: (512) 418-3000

TELEPHONE: (512) 414-7577

INFORMATION FOR EQUINO: 11:

SEQUENCE CRARACTERISTICS:

LENGTH: 4131 base pairs

STRANDESS: 1001

STRANDESS: 1001

STRANDESS: 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 63.1%; Score 198.2; DB Best Local Similarity 79.9%; Pred. No. 1.2e-41 Matches 246; Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Pexas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-08-726-214-11
'Sequence 11, Application US/08726214
'Patent No. 6107076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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90 CCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATGAGCTGCCTCCGGGATGC 149
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5498529-5
;PATENT NO. 5498529
APPLICANT: BERKA, THOMAS R.;FORNWALD, JAMES A.;GORNIAK,
;JOSELINA G.;ROSENBERG, MARTIN.STRICKLER, JAMES E.;TAYLOR, DEAN P.
TITLE OF INVENTION: PROTEIN PROTEASE INHIBITORS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 37.2; DB 6; Length 668; 49.4%; Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37.6; DB 1;
Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,506
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 894,167
FILING DATE: 16-FEB-1989
APPLICATION NUMBER: 897,245
FILING DATE: 16-FEB-1989
APPLICATION NUMBER: 897,245
                                                                                                                      31,705-01
APPLICATION NUMBER: US/08/240,357
FILING DATE: 10-MAY-1994
                                                           Gordon, Alan M.
                                                                                                              REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-324
TELEFAX: 201-831-3305
                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                               12.08;
49.28;
                                                                                                                                                                           TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
                                                                                                                                                                                                                                        LENGTH: 4046 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 CTTCGAAGATACCGAAG 286
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                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 131..3625
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nes 126; Conser
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5498529-5
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Patent No. 5578401
GENERAL INFORMATION:
APPLICANT: Ishikawa, Yoshihiro
TITLE OF INVENTION: Cloning and Characterization of
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.0%; Score 37.6; DB 1; Best Local Similarity 49.2%; Pred. No. 0.52; Matches 97; Conservative 0; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             American Cyanamid Company
                               MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII from DW4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/793,961A
FILING DATE: 19911118
                                                                                                                                                                                                                                                                                                                       31,705
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4046 base pairs listed
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GORGON, Alan M.
REGERENCE/DOCKET NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203 321 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Cyanamid Plaza
CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 CTTCGAAGATACCGAAG 286
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                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 203 321 2971
                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 07470-8426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-240-357-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-793-961A-1
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272 AGGGCCCGCCTGGCGGGGGGGGGGGGGGGCCGCCCGAGCCCAACCGAGTCCGACCAG 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37.2; DB 4; Length 1
Pred. No. 0.55;
); Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 GIGCCCCCTCTCCCCCTAGACCTCAGCTCATTAGCCGCAGCGG 166
                                                                                                                  212 GIGCCCCTCTGCTCGGCCTAGACCTGAGCTCATTAGGCGGCAGCGG 166
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                                                             258 AGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCCGGCGG 304
                                                                                                                                                                                                                                                             Sequence 5, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generacch, Inc.
SIREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORDUTER TANDELS TO THE TANDELS TO T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1438 Base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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47.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                           US-08-828-683A-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-828-683A-5
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                                     CAAGGAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGAC 296
                                                                                                                                                                                                                                                                      138 CCTCCGGGATGCAGAGCCACCCAGCCCCAGCGCGGGCCCCCTCGGTGCCCCTGGCA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGATGACGCCTTCATCCGGAGGGGCGCCCANGCAAGGGCAAGGAACTGGGGCTGCGGGC 257
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                                                                                                                     CCCCCCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCCANGCAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08928069
Patent No. 64621176:
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: App-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Winpatin (Generical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: MARISCHARGY, Diane L.
REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                             297 ACCGGCGGGACCGCT 311
                                                                                                                                                                                                                                                                                                                                                                                                                     TCCGGCCGCNGCNCT 376
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STRANDEDNESS: Single
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US-08-928-069-5/c
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APPLICANT: Daggett, Lorrie P.
APPLICANT: Elis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chin-chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTRO SUBUNITS, DNA
TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2926 AGAGGCCCCCAGGCGCCGGAGAGCCAGGAGCCGTGGCTGTCACAGGGTGGAAGGTGAGGA 2867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 CAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATAIG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 TGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCANGCAAGGCCAAGGAACTGGGGCTG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: US/08/486,273A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
2686 CAGGCGGGCCGGTGCACCCAGCGGGCAGCGGGCTG 2651
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Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
AMME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
                                                                                                              Sequence 44, Application US/08486273A Patent No. 5985586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION TELEPHONE: 619-238-0999
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Best Local Similarity 45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 3243 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: Coding Se
; LOCATION: 1...3243
US-08-486-273A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                    Patent No. 5985586
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 92101-2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                  RESULT 14
US-08-486-273A-44/C
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                                                                                                   APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2806 TGCTGCCAGGCGGGCCCCTGCCTGCTCGCCTGCCAGGCCTCCCGGTAGATCGGC 2747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2926 AGAGGCCCCCAGGCGCGGAGAGCCAGGAGCCGTGGCTGTCACAGGGTGAGGTGAGGA 2867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 CAGAAGCGTTCGCGGCGCCCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 AGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGGCCCCCCTCGGTGCCCC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 TGGCAGGATGACGCCTTCATCCGGAGGGGGGCCCANGCAAGGGCCAAGGAACTGGGGCTG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 AGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGTGAACGCAATGGG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3243;
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 150;
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCCAGTGGCCTGGGCTTCGAAGATACCGAAGTG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.7%; Score 36.6; 45.7%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
                                        Sequence 44, Application US/08231193A Patent No. 5849895 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coding Sequence 1...3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3243 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 126; Conserva
                                                                                                                                                                                                                                                                                                                STREET: 1660 Un:
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                  RY: U.S.A.
92101-2926
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MOLECULE TYPE:
                  -08-231-193A-44/C
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US-08-231-193A-44
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                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Sequence 44, Application US/08480474

Patent No. 6033865

GENERAL INFORMATION:
PAPPLICANT: Bilis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-chun
TITLE OF INVENTION: SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STREET: 0.5.A.
COUNTRY: U.S.A.
ZIP: 92101-2926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.7%; Score 36.6; DB 3; Length 3243; Best Local Similarity 45.7%; Pred. No. 0.89; Matches 126; Conservative 0; Mismatches 150; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REDAMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Parent Persons #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,474
FILLNG DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTONEY/AGENT INFORMATION:
                         2686 CAGGGGGGCCGGTGCACCAGCGGCAGCGAGCTG 2651
253 CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6362-9382B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seddman, Stephanie
REGIETRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-
TELECOMMUNICATION INFORMATION:
TELEPAN: 619-238-0997
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coding Sequence 1...3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3243 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                             RESULT 15
US-08-480-474-44/C
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; LOCATION:
US-08-480-474-44
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Search completed: March 1, 2003, 04:04:35 Job time : 18.6909 secs

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March 1, 2003, 02:24:48 ; Search time 12.892 Seconds
(without alignments)
15188.998 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                     460893 seqs, 311809382 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                    IDENTITY_NUC Gaport 1.0
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Maximum DB seq length: 200000000
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314
                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                      Scoring table:
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/cgn2_6/ptodate/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodate/2/pubpna/USO8_PUBCOMB.seq:* 110 111: 113: 14:

Published_Applications_NA:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1. Appli	ຸ ເກ	10.	Sequence 12, Appl	9	Seguence 165, App	Sequence 487, App	Sequence 12, Appl		Sequence 5, Appli	Sequence 5, Appli		5	Sequence 44, Appl		Sequence 44, Appl	43,	Sequence 43, Appl	43,
a.	US-09-750-240-1	US-09-750-240-5	US-09-750-240-10	US-09-750-240-12	US-10-201-000-1	US-09-933-797-165	US-09-728-445-487	US-09-935-541-12	US-10-081-280-5	US-10-112-793-5	US-10-112-193-5	US-09-884-733-5	US-09-993-234-5	US-09-945-901-44	US-10-007-747-44	US-10-038-937-44	US-09-945-901-43	US-10-007-747-43	US-10-038-937-43
DB	10	10	10	10	φ	σ	10	10	6	σ	σ	10	10	σ	6	6	6	6	6
% Query Match Length DB	314	3549	3552	3582	4942	358	220	6503	1438	1438	1438	1438	1438	3243	3243	3243	3698	3698	3698
Query Match	99.7	94.0	94.0	94.0	94.0	52.0	30.1	12.3	11.8	11.8	11.8	11.8	11.8	11.7	11.7	11.7	11.7	11.7	11.7
Score	313	295.2	295.2	295.2	295.2	163.4	94.6	38.6	37.2	37.2	37.2	37.2	37.2	36.6	36.6	36.6	36.6	36.6	36.6
Result No.	П	7	m	4	S	9	7	ထ	ი ე	c 10	c 11	c 12	c 13	c 14	c 15	c 16	c 17	c 18	c 19

c 20	36.6	11.7	4002	σ	US-09-945-901-53	Seguence 53, Appl
	36.6	11.7	4002	6	-747-5	53
c 22	36.6	11.7	4002	6	US-10-038-937-53	53,
	36.6	11.7	4017	6	-901-4	49,
	36.6	11.7	4017	6	10-007-747-4	49
	36.6	11.7	4017	σ	US-10-038-937-49	49,
	36.6	11.7	4053	6	09-945-901-4	47,
	36.6		4053	6	007-747-4	4
	36.6		4053	6	-4	47,
	36.6		4068	6	•	'n
c 30	36.6	11.7	4068	6	1	'n
	36.6	11.7	4068	σ	038-937	'n
	36.6	11.7	4077	σ	US-09-945-901-51	51,
	36.6	11.7	4077	0	-747	51,
	36.6	11.7	4077	σ	038-937	51,
	36.6	11.7	4092	σ	945-9	45,
	36.6	11.7	4092	σ	007-747-4	45,
	36.6	11.7	4092	σ	-937-4	45,
	36.4	11.6	485	σ	US-10-004-717-59	29,
	36	11.5	22118	δ	US-09-799-462A-16	16,
	36	11.5	22118	σ	US-10-125-767-16	16,
	36	11.5	22118	σ	US-09-815-981-5	വ
	36	11.5	22118	o	7	16,
	5.	11.3	10797	10	US-09-764-847-1577	
	35.2	11.2	2883	σ	Ч	Sequence 157, App
c 45	5.	11.2	2883	6	-758-15	Sequence 157, App
					ALIGNMENTS	
TIS-09-7	KESULT 1 US-09-750-240-1					
; Seque	Sequence 1, Application US/09750240	pplicat	ion US/	0975	0240	
GENER	GENERAL INFORMATION	MATION:	314/AI			
APPL	APPLICANT: HA	Hammon, Insel,	Н. К. Д.			
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
APPLICANT: Insel, P. A.

APPLICANT: Ping, P.
APPLICANT: Post, S. R.
APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: EALLURE
FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/402,667
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1999-12-77
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR PELLOR DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 1
FORCEMENT ON 10 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.7%; Score 313; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.2e-73;
Matches 314; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , LUCATION: (1)...(314); OTHER INFORMATION: n = A,T,C OF G US-09-750-240-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (1)...(314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60

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61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCC 180
181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCCANGCAAGGGCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCCANGCAAGGGCAAG
                          Sequence 10, Application US/09750240

Sequence 10, Application US/09750240

Patent No. US20020103147A1

GABERAL INFORMATION:

APPLICANT: Hammon, H. K.

APPLICANT: Ping, P. A.

APPLICANT: Ping, P. A.

APPLICANT: Post, S. R.

APPLICANT: Goot, S. R.

APPLICANT: GOOT, M.

TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART

TITLE OF INVENTION: GENE THERAPY

FILE REFERENCE: 220002056723

CURRENT APPLICATION NUMBER: US 09/472,667

PRIOR APPLICATION NUMBER: US 09/472,667

PRIOR APPLICATION NUMBER: US 09/472,667

PRIOR APPLICATION NUMBER: US 09/4757

PRIOR APPLICATION NUMBER: US 08/924,757

PRIOR PILING DATE: 1999-10-16

PRIOR PILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: US 08/924,757

PRIOR PRILING DATE: 1997-06-16

PRIOR PRILING DATE: 1997-06-16

PRIOR PRILING DATE: 1997-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 295.2; DB 1 Pred. No. 1.6e-68;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 94.0%;
Best Local Similarity 97.1%;
Matches 300; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                           121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCC 180
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  DB 10; Length 3549;
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APPLICANT: INSEL, P. A.
APPLICANT: Insel, P. A.
APPLICANT: Paig, P.
APPLICANT: Post, S. R.
APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT APPLICATION NUMBER: US/09/750,240
PRIOR FILING DATE: 1999-12-27
PRIOR PELLING DATE: 1999-01-16
PRIOR FILING DATE: 1999-01-16
PRIOR APPLICATION NUMBER: US/08/4,757
PRIOR APPLICATION NUMBER: US/08/24,757
PRIOR APPLICATION NUMBER: US/08/61
PRIOR APPLICATION NUMBER: US/08/61
PRIOR APPLICATION NUMBER: US/08/61
PRIOR APPLICATION NUMBER: US/08/708,661
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Best Local Similarity 97.1%; Pred. No. 1.6e-68;
Matches 300; Conservative 0; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Length 3552;

DB 10;

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61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL TITLE OF INVENTION: CYCLASE
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; Sequence 165, Application US/09933797
; Patent No. US20020155119A1
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
; TITLE OF INVENTION: Sinus Expressed Sequences
; FILE REFERENCE: 9901-007-99
; CURRENT ENTING DATE: 2010-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR PELING DATE: 1999-05/14
; PRIOR FILING DATE: 1999-05/14
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 94.0%; Score 295.2; DB 9; Best Local Similarity 97.1%; Pred. No. 1.7e-68; Matches 300; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                         CURRENT APPLICATION NUMBER: US/10/201,000
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: US/94/14,076
PRIOR FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: PCT/US98/13694
PRIOR FILING DATE: 1999-12-12
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING PATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: human type VI adenylyl cyclase
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
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; LOCATION: (145)..(3648)
US-10-201-000-1
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US-09-933-797-165
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                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hammon, H. K.
APPLICANT: Hammon, H. K.
APPLICANT: Insel, P. A.
APPLICANT: Dost, S. R.
APPLICANT: Gao, M.
TILLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TILLE OF INVENTION: FAILURE
FILE REFERENCE: 220002056723
CURRENT FALLON NUMBER: US/09/750,240
CURRENT FALLON NUMBER: US 09/472,667
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1999-01-16
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR PELLING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 13
COFTWARE: FASTESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.0%; Score 295.2; DB 10; Best Local Similarity 97.1%; Pred. No. 1.6e-68; Matches 300; Conservative 0; Mismatches 9;
                                                                                            Sequence 12, Application US/09750240 Patent No. US20020103147A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 GCCGGGACG 330
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US-10-201-000-1
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Length 4942;

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TELEX: 415/952-9881
TELEX: 910/371-7168
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55.2%;
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 74; Conserv
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US-09-935-541-12
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                                                                                                                                                                                                       TYPE: DNA
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Fatent No. US20020102543A1
GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Sambrowicz, Brian
FILE REFERENCE: LEX-010-USA
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT APPLICATION NUMBER: US 60/168,358
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFWARE: PSACSO for Windows Version 4.0
SEQ ID NO 487
LENGTH: 220
                                                                                                                                                                                                                                                          CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCC 180
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                                                                                                                                                                                                 123 ATGTCATGGTTTAGTGGCCTCCTGGTTCCCAAAGTGGATGAACGGAAAACAGCTTGGGGG 182
                                                                                                                                                             1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                     Score 163.4; DB 9; Length 358;
Pred. No. 3.7e-34;
2; Mismatches 35; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ); DB 10; Length 220; 3.6e-16; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.1%; Score 94.6; D
Best Local Similarity 84.4%; Pred. No. 3.6e
Matches 119; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09935541
Patent No. US20020150911A1
GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
APPLICANT: McGivern, Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CCCCGCTATATGAGCTGCCTC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 CCTCGCTACATGAGCTGCCTC 204
                                                                                         52.0%;
83.1%;
                                                                                     Query Match
Best Local Similarity 83.1'
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
                 ; TYPE: DNA
; ORGANISM: Murine
US-09-933-797-165
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US-09-728-445-487
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LENGTH: 358
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TITLE OF INVENTION: T-TYPE 100 THERED.

TITLE OF INVENTION: T-TYPE 100 THERED.

CURRENT FILING DATE: 300.49 THE SERVENCE THE REPRESENCE THE REPRESENCE THE SERVENCE THE SERVEN
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272 AGGCCCCGCCTGGCGGGCGGGGGGGGGGGCGCCCGAGCCCAACCGAGTCCGACCAG 213
                                          78 GCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGCTTCTGCACGCCCCGCTATATGAGCTG 137
                                                                                    392 GCGGCCGCTGCTCCATAGCCCTCCGACGGCGCCCCAGGGGCTTCCCGGCTCCGTGCTCTC 333
                                                                                                                              138 CCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCCCCTCGGTGCCCCTGGGCA 197
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  Gaps
                                                                                                                                                      198 GGATGACGCCTTCATCCGGAGGGGCGCCCANGCAAGGGCAAGGAACTGGGGCTGCGGGC
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  0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                258 AGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCGGCGG 304
                                                                                                                                                                                                                                                                                                                                          212 GIGCCCCCTCTGCTCGGCCTAGACCTGAGCTCATTAGGCGGCAGCGG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37.2; DB 9;
Pred. No. 0.55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/112,193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P1052R1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 28-Mar-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10112193 Publication No. US20030004313A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/952-9881
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LENGTH: 1438 base pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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Best Local Similarity 47.6
Matches 108; Conservative
  Conservative
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  Matches 108;
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                                                                                                                                                                                                                                                      78 GCGTTCGCGGCGCCGTGGCACTCGGGCAGTGGCTTCTGCACGCCCCGCTATATGAGCTG 137
                                                                                                                                                                                     392 GCGGCCGCTGCTCCATAGCCCTCCGACGGGCCCCCAGGGGCTTCCCGGCTCCGTGCTCTC 333
                                                                                                                                                                                                                                138 CCTCCGGGATGCAGACCAACCCAGCCCCACCCTGCGGGCCCCCCTCGGTGCCCCTGGCA 197
                                                                                                                                                                                                                                                                                                                    198 GGATGACGCCTTCATCCGGAGGGCCGCCCANGCAAGGCCAAGGAACTGGGGCTGCGGGC 257
                                                                                                                                                                                                                                                                                                                                                          272 AGGGCCCGCCTGGCGGGGGGGGGGGGGGGCCGCCCGAGCCCAACCGAGTCCGACCAG 213
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                                                              Length 1438;
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                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    258 AGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCGGCGG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS: ADDRESSER.
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                                                                                                        119;
                                                           DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.2; DB 9;
Pred. No. 0.55;
                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P1007P1
                                                           Score 37.2;
Pred. No. 0
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10112793 Publication No. US20020192729A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1438 base pairs
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47.6%;
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SEQUENCE CHARACTERISTICS
                                                         11.8%;
ilarity 47.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic Acid
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Best Local Similarity
                                                                                  Similarity
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                                                                                                   Matches 108;
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US-10-081-280-5
                                                              Query Match
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212 GIGCCCCTCTGCTCGCCTAGACCTCATTAGGCGCGCAGCGG 166
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132 TGCCCGTCGTGGTTCCGCCTTCAGCCCCGCCGCCGCCGCCGCCGCCGCGGAA 273
                                                                                 272 AGGCCCCCTGCCGGGGGGGGGGCCCCCCGACCCAACCGAGTCCGACCAG 213
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                                                                                                                                    258 AGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCGGCGG 304
                                                                                                                                                                           212 GIGCCCCCTCTGCTCGCCTAGACCTGAGCTCATTAGGCGGCAGCGG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 AGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCGGCGG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; DB 10;
0.55;
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 Ligand Inhibitor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.8%; Score 37.2; D
Best Local Similarity 47.6%; Pred. No. 0.55
Matches 108; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,733
FILING DATE: 19-Jun-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MAISCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REBERENCE/DOCKET NUMBER:
TELEPHONE: 415,225-5416
TELEFAX: 415,922-9881
TELETAX: 910,371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

**PAPLICATION WUNBER: 09/304,003

**FILING DATE: 14-JUNE-2000

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-884-733-5
                                                                                                                                                                                                                                                                       Sequence 5, Application US/09884733 Patent No. US20020123116Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1438 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                       RESULT 12
US-09-884-733-5/c
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78 GCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGCTTCTGCACGCCCCGCTATATGAGCTG 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 AGGCCCGCCTGGCGGGGGGGGGGGGGCCCCCGAGCCCAACCGAGTCCGACCAG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACGACGCGGG 304
                                                                                        APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; DB 10;
0.55;
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37.2; DB 10;
Pred. No. 0.55;
0; Mismatches 119;
                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
NAME: MATSCHANG, Diane L.
REGISTRATION WUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: Linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-993-234-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/828,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/09945901 Patent No. US20020161215A1
US-09-993-234-5/c; Sequence 5, Application US/09993234; Patent No. US20020146768A1; CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1438 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415/952-988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.8%;
Best Local Similarity 47.6%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        STATE: California
                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94080
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US-09-945-901-44/C
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HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2866 CAGACAGCCCCCCAGCACAATGGCAGGTGGGCGTGCGGCGTGCAGACGTGCTGTCTG 2807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2806 TGCTGCCAGGCGGGGCCCCTGCCTGCTCGCCTCCTGGCAGGCCTCCCGGTAGATCGGC 2747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2926 AGAGGCCCCCAGGCGCCGGAGAGCCAGGAGCCGTGGCTGTCACAGGGTGGAAGGTGAGGA 2867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 CAGAAGCGTTCGCGCCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCCCCTCGGTGCCCC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGTGAACGCAATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; DB 9;
0.92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/648,797
FILING DATE: 28-Aug-2000
APPLICATION NUMBER: US/08/940,086A
FILING DATE: 29-SEPT-97
APPLICATION NUMBER: US 08/231,193
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1994
FILING DATE: 20-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9383C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/007,747 FILING DATE: 07-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1...3243
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 450-8400
TELEFAX: (619) 450-8499
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                      Sequence 44, Application US/10007747 Patent No. US20020161193A1 GENERAL INFORMATION:
                                                                                                                                                                                                            APPLICANT: Daggett, Lorrie P. Ellis, Steven B. Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3243 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
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STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                  Lu, Chin-Chun
TITLE OF INVENTION: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.7%;
Best Local Similarity 45.7%;
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
                                                                        JS-10-007-747-44/C
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                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                       TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2926 AGAGGCCCCCAGGCGCCGGAGAGCCAGGAGCCGTGGCTGTCACAGGGTGGAAGGTGAGGA 2867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 CAGAAGCGTTCGCGGCGCCCGTGGCACTCGGGCAGGGGCTTCTGCACGCCCCGCTATATG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCCCCTCGGTGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREEF: 4250 Executive Square, 7th Floor
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERROCE/DOCKET NUMBER: 6362-9383E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/945,901
FILING DATE: 24-Jan-2001
CLASSIFICATION: <a href="https://ducarray.com/">ducassification</a>: <a href="https://ducasray.com/">ducassification</a>: <a href="https://ducasray.com/">ducas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1...3243
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/940,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
                                    APPLICANT: Daggett, Lorrie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3243 base pairs
                                                                     Ellis, Steven B.
Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                      Chin-Chun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.73
Best Local Similarity 45.73
Matches 126; Conservative
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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Search completed: March 1, 2003, 09:03:39
Job time: 19.892 secs

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1 atgtcatggtttagtggcct.....acaccggcgggaccgctgaa 314
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                     3936061 segs, 852009584 residues
                                                                                     OM nucleic - nucleic search, using sw model
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                        Scoring table:
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Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

/cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq:* Pending_Patents_NA_New:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	. 8000000000000000000000000000000000000	Sequence 157, App
SUMMARIES	10.226-254A-10.127-128-128-128-128-128-128-128-128-128-128	US-10-194-486-157
DB		9
Length	2883 2883 36303 36303 36303 36303 1878 1878 1878 1878 1878 1878 1824 1824 1824 1824 1824 1824 1824 182	2883
% Query Match	0477233333333333333333333333333333333333	11.2
Score	010 010 010 010 010 010 010 010	δ.
Result No.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

Sequence 3, Appli Sequence 65, Appli Sequence 167, Appli Sequence 1, Appli Sequence 1, Appli Sequence 23402, Ap Sequence 179, Appli Sequence 174, Appli Sequence 131, Appli
PCT-USO2-32117-3 US-10-271-697-3 US-10-271-697-3 PCT-USO2-38445-65 US-09-513-999C-21648 PCT-USO2-32117-1 US-09-949-002-652 US-10-144-771-23402 US-10-094-886-179 US-10-094-886-179 US-10-240-851-66 US-10-144-771-257 US-10-144-771-26872 PCT-USO2-31358-143 US-00-724-656-1374 US-09-724-676-14604
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ALIGNMENTS

PCT-US02-36759-83

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APPLICANT: ZHENG, Wenjin
APPLICANT: GAO, Jing
TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
FILE REFERENCE: PF-1279 PCT
CURRENT APPLICATION NUMBER: PCT/US02/36759
Sequence 83, Application PC/TUS0236759 GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                         BECHA, Shanya D.
YUE, Henry
LEHR-MASON, Patricia M.
THANGAVELU, Kavitha
                         DUGGAN, Brendan M.
YANG, Junming
                                                                     GIETZEN, Kimberly J.
LEE, Soo Yeun
TANG, Y. Tom
AZIMZAI, Yalda
                                                                                                                                                                                                                                  LEE, Sally
EMERLING, Brooke M.
KABLE, Amy E.
KHARE, Reena
BAUGHN, Mariah R.
GANDHI, Ameena R.
TRAN, Uyen K.
RICHARDSON, Thomas W
                                                                                                                                                                                                                                                                                                                                                                                                                        KALLICK, Deborah A. GRIFFIN, Jennifer A. ELLIOTT, Vicki S. GORVAD, Ann E. HAFALIA, April J.A. ISON, Craig H. JIN, Pei
                                                                                                                                                                                                                                                                                                                                                  MARQUIS, Joseph P.
LAL, Preeti G.
FORSYTHE, Ian J.
LEE, Ernestine A.
SWARNAKAR, Anita.
                                                                                                                                WALIA, Narinder K. WARREN, Bridget A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BURRILL, John D.
BLAKE, Julie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JACKSON, Alan
BHATIA, Umesh
                                                                                                                                                               BARROSO, Ines
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APPLICANT:
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1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
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Best Local Similarity 55.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-724-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5921, Application US/10144771
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF THYONION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: CL001321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 5921
LENGTH: 5826
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                                                                                                                                                                                                                                                                                                                                                             Query Match 94.0%; Score 295.2; DB 1
Best Local Similarity 97.1%; Pred. No. 1.6e-65;
Matches 300; Conservative 0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 199.2; DB
Pred. No. 4.3e-41
0; Mismatches 4
                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506194CB1
PCT-US02-36759-83
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/333,097
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/340,542
PRIOR FILING DATE: 2001-12-14
PRIOR PILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2002-01-11
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE: 2002-01-14
SOFTHARE OF SEQ ID NOS: 94
SED ID NO 83
LENGTH: 1386
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Best Local Similarity 82.3
Matches 241; Conservative
                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 GGCGGGACG 333
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; ORGANISM: HUMAN
US-10-144-771-5921
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Db 34505 GAGTGCGGGGCCCCGGCGGGAGTGGGCGGGAGCCTCCCCTACCCCTACCCCCGACCGGCAG 34446
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                                                                                                                                                                                                                                                                            CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCC 180
                                                                                                                                                                                                     213 CCTCGCTACATGAGCTGCCTCAAGAATGCGGAGCCACCCAGCCCCACTCCTGCAGCTCAC 272
                                                                         GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 GCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGCTTCTGCACGCCCCGCTATATGAGCTG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
96 ATGTCATGGTTTAGTGGCCTCCTGGTTCCCAAAGTGGATGAACGGAAAAAACAGCTTGGGGG
                                                                                                    138 CCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCCCTCGGTGCCCCTGGCA
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                                                                                                                                                                                                                                                                                                                                                                                   Length 36303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-152-724A-24/C
Sequence 24, Application US/10152724A
Sequence 24, Application US/10152724A
GENERAL INFORMATION:
APPLICANT: LITTLE, Melissa
APPLICANT: YAMADA, Toshiya
APPLICANT: YAMADA, Toshiya
APPLICANT: WILKINSON, Lorine
APPLICANT: WILKINSON, Lorine
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
SEQUERAL INFORMATION:
APPLICANT: LITTLE, Melissa
APPLICANT: HOLMES, Gregory
APPLICANT: KOLLE, Gabriel
APPLICANT: YAMADA, TOSHIYA
APPLICANT: WILKINSON, LOSHIYA
APPLICANT: TERERENCE: P22378
FILE REFERENCE: P22378
CURRENT APPLICATION NUMBER: US/10/152,724
CURRENT APPLICATION NUMBER: US/10/152,724
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: Australian App No PQ 4348
PRIOR FILING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
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US-10-218-140-5849
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NAME/KEY:
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US-09-724-676-33617/c
US-09-724-676-33617/c
Sequence 33617, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD:
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen,
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 33617
LENGTH: 1878
FILE REFERENCE: P22378
CURRENT APPLICATION NUMBER: US/10/152,724A
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: Australian App No PQ 4348
PRIOR FILING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
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Pred. No. 1.9;
0; Mismatches 149;
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Best Local Similarity 46.09
Matches 127; Conservative
                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-152-724A-24
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US-09-724-676-33617
                                                                                                                       SEQ ID NO 24
LENGTH: 36303
                                                                                                                                                           TYPE: DNA
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RESULT 6

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GENERAL INFUGEATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES AND POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 15966-543 CON
CURRENT APPLICATION NUMBER: US/10/218,140
CURRENT APPLICATION NUMBER: US/10/218,140
FILE REFERENCE: 15966-543 CON
FRICH APPLICATION NUMBER: 09/12,763
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-02
PRIOR PRILING DATE: 1999-04-02
PRIOR PRILING DATE: 1999-04-02
PRIOR PRILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 6322
SOFTWARE: CURANALOR VERSION 1.0
SEQ ID NO 5849
US-09-724-676A-33617/c

Sequence 33617, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILE DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SEQ ID NO 33617

LENGTH: 1878
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LOCATION: (1)...(1)
OTHER INFORMATION: "n" = "a", "c", "t" or "g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5849, Application US/10218140 GENERAL INFORMATION:
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FEATURE:
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; ORGANISM: Homo sapiens
US-09-724-676A-33617
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137 GCCTCCGGGATGCAGAGCCACCCAGCCCCAGCCCTGGGGGCCCCCTCGGTGCCCCTGGC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION UNMBER: US/09/724,676 CURRENT APPLICATION UNMBER: 02/09/724,676 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SECTION 33618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 38.2; DB 6;
llarity 53.4%; Pred. No. 2.1;
Conservative 0; Mismatches 69;
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                                                                            | CCATION: (961)...(961)
| COTHER INFORMATION: "n" = "a", "c", "t" or
| FEATURE: misc_feature
| LOCATION: (1191)...(1191)
| COTHER INFORMATION: "n" = "a", "c", "t" or
| FEATURE: (1193)...(1193)
| COCATION: (1193)...(1193)
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| COCATION: (1193)...(1193)
| US-10-218-140-5849
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FEATURE:
NAME/KEY: misc_feature
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; ORGANISM: Homo sapiens
US-09-724-676-33618
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Matches 79; Conserva
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APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Abo, Qing
APPLICANT: Mulero, Julio J
APPLICANT: William Date: 2000-01-21
PRIOR FILING DATE: 2000-01-22
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-01-2-63
PRIOR FILING DATE: 2000-01-2-63
PRIOR FILING DATE: 2000-01-2-63
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR APPLICATION NUMBER: PCT/USO1/03800
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                                                 APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 12181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                    Score 38.2; DB 5;
Pred. No. 2.1;
0; Mismatches 149;
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Sequence 33618, Application US/09724676A GENERAL INFORMATION:
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Best Local Similarity 46.0%;
Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-724-676A-33618
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Best Local Similarity
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LENGTH: 3182
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APPLICANT: Bellen, Hugo
APPLICANT: Bellen, Hugo
APPLICANT: Bermingham, Nessan
APPLICANT: Bermingham, Nessan
APPLICANT: Bermingham, Nessan
APPLICANT: Ben-Arie, Nissim
TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-associa
TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-associa
TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-associa
TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-associa
TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-associa
TITLE OF INVENTION NUMBER: US 60/137,060
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1000-01-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 GCTTCTGCACGCCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCCAGCCCCACC 169
                                                                                                                                                                                                                                                                                                                                                                                                                              70 GGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTAT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        821 GGGCGCTGGCCTCGCGGGCGGGCTCGGGCTGCAGCGGCTCCTTCGGGGCCTCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 CTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCGGCGGG 305
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11.6%; Score 36.4; DB 5; Length 485;
Best Local Similarity 54.7%; Pred. No. 4;
Matches 70; Conservative 0; Mismatches 58; Indels (
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                              Score 36.6;
Pred. No. 5;
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: LOCATION: (147)...(147)

OTHER INFORMATION: n can be any nucleotide

US-09-585-645A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-585-645A-59/c; Sequence 59, Application US/09585645A; Sequence 59, Application US/09585645A; APPLICANT: Zoghbi, Huda
  SOFTWARE: PatentIn version 3.1
SEQ ID NO 347
LENGTH: 2216
                                                                                                                                                                                                                                                                                                              11.7%;
47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 70 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                      Matches 111; Conservative
                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                           ; LOCATION: (1)..(1542); OTHER INFORMATION: PCT-US02-38526-347
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: CHICKEN
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SOFTWARE: Pates
SEQ ID NO 59
                                                                                                                                          FEATURE:
NAME/KEY: CDS
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CURRENT PELLING DATE: 2002-12-03
PRIOR PAPLICATION NUMBER: US 09/488,725
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR PELLING DATE: 2000-10-21
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-25
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-02-13
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-06-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 GGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTAT 129
                 PRIOR APPLICATION NUMBER: US 09/598,075
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2.001-02-05
PRIOR FILING DATE: 2.001-02-05
NUMBER OF SEQ ID NOS: 653
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 CTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCGGCGGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641 GAGGGCTCAGGCTCCACGAGGGCCGCGCCACAGCGCCCACGTCGCCAAGG 586
                                                                                                                                                                                                                                                                                                                                                                                             11.7%; Score 36.6; DB 1; Length 1542; 47.0%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 347, Application PC/TUS0238526 GENERAL INFORMATION:
PRIOR FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ghosh, Malabika
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Zhiwei
APPLICANT: Zhao, Qing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu, Chongjun
Mulero, Julio J
Boyle, Bryan J.
                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 47.0 Matches 111; Conservative
                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
PCT-US02-38526-347/c
                                                                                                                                                                                                                                                                                                                                     PCT-US02-38526-349
                                                                                                                                                                                                                            SEQ ID NO 349
                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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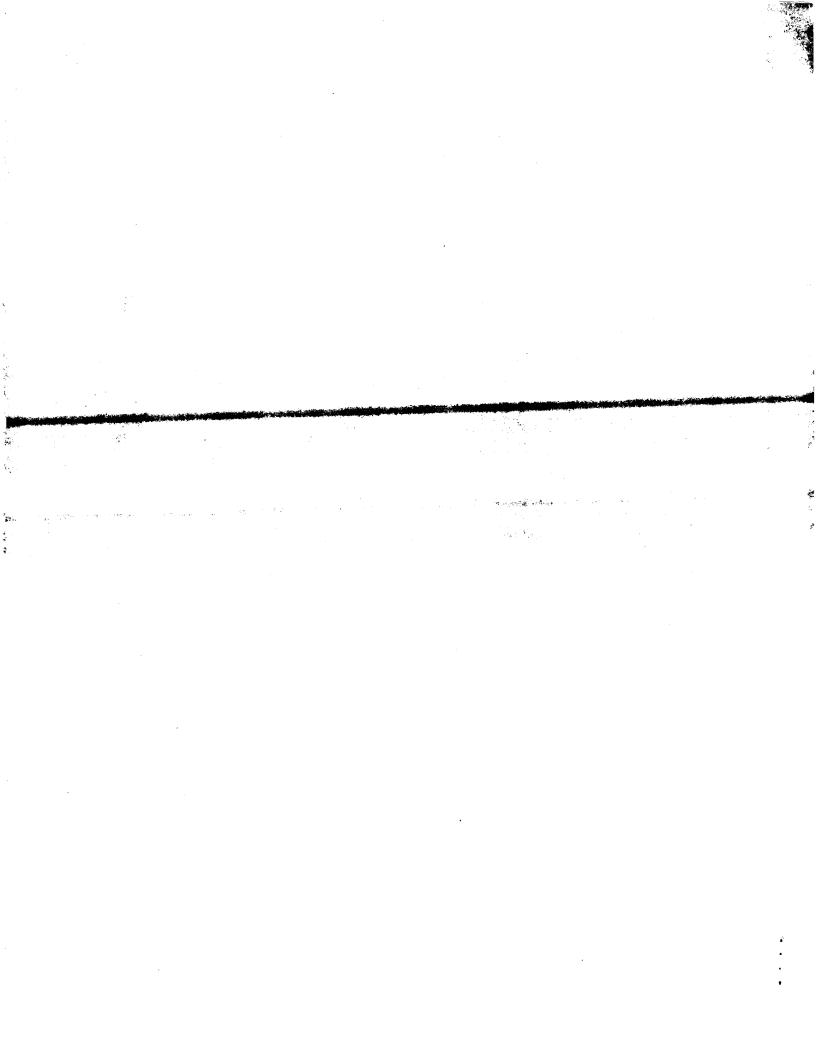
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1514 CCCCCCAAAAAGGCAGGCAAGCCGCTGGGCGGTGGGACGTCACCACCGCAGGAAATCGCG 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 CAGGTGGCTTCTGCACGCCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                       160 AGCCCCACCCCTGCGGGCCCCCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGG
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 45770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45770, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LT
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.8;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                    US-09-724-676-45770/c
; Sequence 45770, Application US/09724676
; GENERAL INFORMATION:
                                                                                                                                                                                                           13319 AGGGAGGGACGGACGGACGCGGGAC 13295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1454 AATGAACTTCCAGAGCTTGGTGACC 1430
                                                                                                                                                                220 GGCGGCCCANGCAAGGCAAGGAAC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 AAGTGACAACGACACCGGCGGGACC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1515)..(1516)
OTHER INFORMATION: n is a,c,g, or
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; LCCATION: (1528)..(1528)
; OTHER INFORMATION: n is a,c,g,
US-09-724-676-45770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1525)..(1525)
OTHER INFORMATION: n is a,c,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.48;
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NAME/KEY: misc_feature
LOCATION: (1522)..(1522)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-724-676A-45770/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                        AFFLICANT: nautacony, Jadar
Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 CGGCAGGTGGCTTCTGCACGCCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCC 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 6; Length 22118;
Pred. No. 12;
0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/287,313
FILING DATE: 01-Nov-2002
CLASSIFICATION NUMBER: 09/724,726
FILING DATE: 10-APP.1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 10-APP.1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 10-ARG-1996
APPLICATION NUMBER: 08/695,191
FILING DATE: 11-ARG-1996
APPLICATION NUMBER: 08/695,191
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/692,080
FILING DATE: 10-ARG-1996
APPLICATION NUMBER: 08/692,080
FILING DATE: 10-ARG-1996
APPLICATION NUMBER: 08/699,822
FILING DATE: 10-ARG-1996
APPLICATION NUMBER: 08/6196
APPLICATION NUMBER: 08/6196
APPLICATION NUMBER: 08/6196
APPLICATION NUMBER: 08/6196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6869-402N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-287-313-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 22118 base pairs
                                                                                                                                                                                   Sequence 16, Application US/10287313 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: «Unknown>
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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ilarity 48.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                              APPLICANT: Hadlaczky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'ELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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les 99; Conserv
                     230 GCAAGGGC 237
                                                                   133 CCACGGGC 126
                                                                                                                                      RESULT 13
US-10-287-313-16/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.4%; Score 35.8; DB 5; Length 1824; Best Local Similarity 47.3%; Pred. No. 7.6; Matches 97; Conservative 0; Mismatches 108; Indels 0;
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID 45770
LENGTH: 1824
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1515)...(1516)
OTHER INFORMATION: n is a.c.g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1522)...(1525)
OTHER INFORMATION: n is a.c.g, or t
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846 932 950 778 925	935 968 1075 1010	1203 884 948 486	894 1612 1101	844 844 844	935	731	1538 717 858	1003	4447 581 587	500 687 725 839 504		IKEN fu	GI:17.	us Metazoa Eutheria 1 to 611	Araka, Hiram Kawa	, Sakai , Shina ashi,F.	A., Ya.	0 40 5 40
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5.1.3 Compugen Ltd.	; Search time 301.551 Seconds (without alignments) 16864.108 Million cell updates/sec	acaccggcgggaccgctgaa 314		idues .	ters: 32308132										results predicted by chance to have a to the score of the result being printed, of the total score distribution.		Description	BB866520 BB866451 BB866451 AL212334 Tetraodon BG916212 602814927 AL053013 Drosophil AL098882 Drosophil
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), (strain=C3H, tissue_type=brain, cell_line=CRL-1443)
                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer based methods for the mouse full-length cDNA
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             Email: genome_resegsc.riken.go.jp,
URL:http://genome_gsgsc.riken.go.jp,
Carninci.P., Shibata,Y. Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 611)
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
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Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Takahira, S., Tanakaya, T., Tomaru, T., Towaru, Y., Watahiki, A., Yasanishi, A., Muramatsu, M. and Hayashizaki, Y.
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Normalization and subtraction of cap-trapper-selected cDNAs to
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penes. Genome Res. . 10 (10), 1617-1630 (2000)
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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Hayashizaki,Y.
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Contact: Yoshinide Hayashizaki
Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Paris 1-722 Suchino-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
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Computer-based methods for the mouse full-length cDNA
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                     (tissue_type=bone marrow, cell_type=stroma cell,
cell_line= CRL-2028 SR-4987), (tissue_type=colon,
cell_line=CRD-142 RAG), (tissue_type=stroma-tine-tine=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=CRL-1669 BCLI Clone 13.20-3B3
), (strain=C3H, tissue_type=brain, cell_line=CRL-1443
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Submitted (12-ARR-2000)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                              1;
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Tetracdon nigroviridis.

Tetracdon nigroviridis.

Tetracdon nigroviridis

Tetracodon nigroviridis

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetracodontiformes;

Tetracodontidae; Tetracodon.

1 (bases 1 to 1011)

Ross: To 1011)

Ross: To 1011)

Ross: To 1011)

Ross: To 1011

Ross: To 101
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(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
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Pred. No. 1.9e-34;
0; Mismatches 61; Indels
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ilarity 78.2%;
Conservative
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 151.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 ATGTCCTGGTTCAGTGGTTTCCTAGTGGCCAGAGTGGACGACGAAAGAGCGCCTGGGGG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                          /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="152F16"
/clone="lib="G"
/oroscope sequence ID : COAG162DC08SP1-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT
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                                                                                                                                                                                                                                                                                                                                    Score 60.2; DB 17; Length 1011;
Pred. No. 9.1e-05;
1; Mismatches 64; Indels 10;
                                                                                                                                                                                                                                                          24 others
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//tissue_type="tumor, gross tissue"
dev_stage="5 months"
/lab_host="DH108"
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
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63.1%;
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Matches 128; Conservative
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Query Match
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CNS010EW/c
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               providing samples: Lothar Hennighausen/Priscilla Furth, with Reference for transpenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996) " 234 c 131 g 189 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSO091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Library constructed by Life Technologies. Investigators
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                                                                                                                                                                                                                                                           12 ATGTCATGGTTGAGAGGGCTCCTGGATTCCCAAACGTGGATGAACGGAAAACACGCTTGGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                   1 ATGTCATGGTTTAGTGGCCTCCTGG--TCCCTAAAGTGGATGAACGGAAAACAGCCTGGG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GTGGATGAACGGAAAACAGCCTGGGGTGAACGCAATGGGCAGAAGCGTTCGCGGCGCCGT
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                                                                                                                                              ch 18.7%; Score 58.8; DB 13; Length 941; I Similarity 84.8%; Pred. No. 0.0002; 78; Conservative 0; Mismatches 12; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 925;
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/db_xref="taxon:7227"
/clone="BACR19D16"
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llarity 15.8%; Pred. No. 0.013;
Conservative 126; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                  GTGAACGCAATGGGCAGAAGCGTTCGCGGCGC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fly), genomic survey sequence.
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/note="end : TET3"
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                Query Match
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CNS0091P/c
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                                                                                  BASE COUNT
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TITLE
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KEYWORDS
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACNO3F19 of DrosBAC library from Drosophila melanogaster (fruit AL098882
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                              116 GCACGCCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCTGCGG 175
94 GGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATGAGCTGCCTCCGGGATGCAGAG 153
                                                                                                                                           214 CGGAGGGCGCCCCANGCAAGGGCAAGGAACTGGGGCTGCGGCCAGTGGCCCTGGGCTTC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 GGGGTGAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCT 115
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 CCACCCAGCCCCACCCCTGCGGGCCCCCTCGGTGCCCCTGGCAGGATGACGCCTTCATC
                                                                                         176 GCCCCCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCANGCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 others
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                                                                                                                                                                                                                                       274 GAAGATACCGAAGTGACAACGACACGGGGGGGGGCCGCT 311
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/db_xref="taxon:7227"
/clone="BACN03919"
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178 g
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377 c
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us-09-750-240-1.rst

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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.ouffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ948546 1502 950 bp mRNA linear EST 21-AUG-2002 AGENCOURT_8841400 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6199251 5', mRNA sequence.
                                                                                                                                                                                                                                                                  Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 932)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 GCCTGGGGTGAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 TTCTGCACGCCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTT
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/db_xref="taxon:7227"
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32.7%; Pred. No. 1...
'''e 49; Mismatches
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          genomic survey sequence.
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/note="end : T7"
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                                                                                                  Drosophila melanogaster
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                                                  AL066742.1 GI:4945205
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Matches
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                                                                                                                                           CNSO10RJ 846 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACNO4N13 of DrosBAC library from Drosophila melanogaster (fruit
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC ibrary (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Cenevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 GCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATGAGCTGCCTCCGGGATG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 SSSASSASSSSSSSSAAASAAGASSVSSASSAVSSSSSSASAASSSASASVSSSSSVS 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 TCATCCGGAGGGCCGCCCANGCAAGGCAAGGAACTGGGGGCTGCGGGCAGTGGCCCTGG 268
                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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284 others
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/db xref="taxon:727"
/clone="BACN04N13"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                                                                                                                                              11y), genomic survey sequence. AL099337
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
1 (hases 1 to 778)
1 (hases 1 to 778)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dr priming. Directionally cloned using the following adaptors:
                                                                                                                                                                       Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 572.
Location/Qualifiers
1 (bases 1 to 950)
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.6;
0; Mismatches 56; Indels
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/organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="InMaGE:6199251"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Email: cgapbs-r@mail.nih.gov
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Matches 73; Conservative
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925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley brosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="epidermoid carcinoma, cell line"
/lab_host="NH10B (phage-resistant)"
/note="Corgan: lung; Vector: poTB7; Site_1: EcoRI; Site_2:
/note="Corgan: lung; Vector: poTB7; Site_1: EcoRI; Site_2:
/note corgan: lung; Vector: poTB7; Site_1: CDN and by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAGG(5). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NHLMGC Library."
                        CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage-llnl.gov
Plate: LLCM2608 row: j column: 06
High quality sequence stop: 481.
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6425957"
/clone_lib="NIH_MGC_101"
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lissue Procurement: ATCC
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more dettailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 AGAAGCGTTCGCGCCCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATGA 133
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/db_xref="taxon:7227"
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Pred. No. 2.2;
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/clone_lib="RPCI-98"
/note="end : TET3"
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10.4%;
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/organism="Drosophila melanogaster"

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Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the Berkeley prosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                               75 GAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATGAG 134
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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/db_xref="taxon:7227"
/clone="BACR14N09"
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                        /clone="BACN03J03"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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203 ACGCCTTCATCCGGAGGGGCGGCCCANGCAAGGCAAAGGAACTGGGGGCTGCGGGCAGTGG 262
                                                                   GGGATGCAGAGCCACCCAGCCCCACCCTGCGGGCCCCCCTCGGTGCCCCTGGCAGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-A0G-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the RsD process and may have higher chance of
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Pan troglodytes
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Pan troglodytes DNA, clone: PTB-003A16.F, genomic survey sequence.
AG030603
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                               83 CGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATGAGCTGCCTCC 142
                                                                                                                                               801 GCGCGSGSGCGGCGGGSSSGGSGSCCGSCGGGCGSSCSCSCCGCGSGSSCS 860
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BAC end sequences of Library PTB
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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                 Length 935;
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/clone_lib="PTB Chimpanzee Male BAC Library"
361 c 474 g 16 t 77 others
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Pred. No. 3.2;
0; Mismatches 111;
                 DB 17;
                                              73;
             13.3%; Score 41.8; Dilarity 36.7%; Pred. No. 3.2; Conservative 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-003A16.F"
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R.Site 1 : Saci
R.Site 2 : Saci.
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Best Local Similarity 48.8%;
Matches 106; Conservative
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CGSGGCGS 868
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Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-065P04.F.
Pan troglodytes
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (6SC);
1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:s181-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                        AG073983 1075 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-065P04.F, genomic survey sequence.
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Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
388 c 553 g 18 t 61 others
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Pred. No. 4.1;
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CGCGCCGCGGNGAGCGCGGAGCGACGACAAAAC 952
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/organism="Pan troglodytes"
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R.Site 2 : SacI.
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            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compuc
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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AR174471 Sequence AX189757 Sequence

Description

ACO74028 Mus muscu LO1115 Rattus norv ACO74028 Mus muscu LO115 Rattus norv ACO96835 Rattus no M96653 Mus musculu U72484 Fugu rubrip AC126672 Mus muscu ACO98456 Rattus no AFO7709 Streptomy AL445945 Streptomy ACO97157 Rattus no L36825 Mus Musculu J02220 Herpes simp AF157643 Mycobacte AC099455 Rattus no AC090051 Homo sapi AL442109 Oryza sat AL662984 Oryza sat ACO91123 Oryza sat AP003328 Oryza sat AP002843 Oryza sat AE006014 Caulobact AB007882 Homo sapi AF25226 Homo sapi AC021647 Homo sapi AC117498 Homo sapi AC02557 Homo sapi M9468 Camins famil 129958 Sequence AC115355 Mus muscu AC091123 Oryza sat V00462 Herpes simp AF288483 Azospiril M96160 Rattus norv Oryza sat Caulobact Sequence Ralstonia AX305965 Sequence AL662976 AE005839 AL646064 B AX189766 AC126672 AC098456_0 AF072709 MUSALCR01 AC115355 AC091123 HEHS03 AF288483 HS11EM5G AF157643 AC099455 AC097157 AP002843 В1011H02 U72484 10 99.6 99.6 314 95.6 3529 95.6 95.6 95.6 95.6 95.6 95.6 95.6 95.6 95.6 95.6 95.6 96.3 9 103.5 103.5 103.5 103. 103 100 99.5 99 99 0000 00000

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 314)
Hammond, H.K. and Gao, M.
Gene therapy for congestive heart failure
Patent: WO 0148164-A 1 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
                                                                                                                                                                                                                                                                                                               GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro 100
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                                                                                 1 (bases 1 to 314)
Hammond, H.Kirk., Insel, P.A., Ping, P., Post, S.R. and Gao, M. Gene therapy for congestive heart failure
Patent: US 6306830-A 1 23-CCT-2001;
Location/Qualifiers
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/organism="unknown"
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                                                                                             181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCCANGCAAGGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 3549)
Hammond, H. Kirk., Insel, P.A., Ping, P., Post, S.R.
Gene therapy for congestive heart failure
Patent: US 6306830-A 5 23-OCT-2001;
Location/Qualifiers
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Length:
Matches:
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Matches:
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Sequence 5 from patent US 6306830.
ARI74473
ARI74473.1 GI:17914793
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                                                                          US-09-750-240-2 (1-104) x AX189757 (1-314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
1025 c 1061 g
3.27e-29
568.00
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99.65%
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                     Percent Similarity:
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Db 301 GGCGGG 306	RESULT 5 AX189766 LOCUS AX189766 3552 bp DNA linear PAT 08-AUG-2001 DEFINITION Sequence 10 from Patent WO0148164.	AA103/00.1 GI:LJ143139 human. 1 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 3552) AUTHORS Hammond, H.K. and Goo, M. TITLE Gene therapy for congestive heart failure JOURNAL Patent: WO 0148164-A 10 05-JUL-2001;	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) FEATURES 1. 3552 Source 1. 3552 "Homo sapiens" //Organism="Homo sapiens" /db_xref="taxon:9606" 761 t ORIGIN	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Ouery Match: Conservative: Op.06% Mismatches: Ob: Conservative: Op.06% Mismatches: Ob: Conservative: Op.06% Mismatches: Op.06%	US-09-750-240-2 (1-104) x AX189766 (1-3552)	Oy 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20	Qy 21 GluargasnGlyGlnLysargSerargargGlyThrargalaGlyGlyPheCysThr 40	<pre>Qy 41 ProargTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60 </pre>	<pre>Qy 61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80 </pre>	Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro 100 	Qy 101 AlaGly 102 1 1 Db 301 GGCGG 306	AX189768 3582 bp	TION Sequence 12 from Patent ION AX189768 N AX189768.1 GI:15143140 DS	_	TITLE Gene therapy for congestive heart failure JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;
Db 61 GAACGCAATGGGCAAGAGCGTTCGCGGCGCGCGCACGTGGCAGGTGGCTTCTGCACG 120	Oy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60		241 101 301	RESULT 4 AX189761 3549 bp DNA linear PAT 08-AUG-2001 DEFINITION Sequence 5 from Patent WO0148164. ACCESSION AX189761. GI:15143135	SOURCE human. ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 3549) AUTHORS Hammond, H.K. and Gao, M. TITLE Gene therapy for congestive heart failure	JOURNAL PATENT: WO 0148164-A 5 05-JUL-2001; THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) FEATURES LOCATION/Qualifiers	ource	i	1.00	Gaps: 0-2 (1-104) x AX189761 (1-3549)	Oy 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20	Oy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40	Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60	Qy 61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80	QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro 100 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	101 AlaGly 102

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission Submission Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (F-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914) On May 9, 2002 this sequence version replaced gi:2887418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishikawa,K., Nagase,T., Nakajima,D., Seki,N., Ohira,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes.
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                                                                                                                                                                                                                                                                                                                 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro 100
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Homo sapiens
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THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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99
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          Location/Qualifiers
1. 3582
1. 61. 3582
1. 7.0ganism="synthetic construct"

/db_xref="taxon:32630"

/note="Modified AC-VI"

a 1036 c 1067 g 776 t
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Mismatches:
Indels:
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Ohara, 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256
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Matches:
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OSCEVANVRASIANFSEFYVELEANNEGVECLRLLAEIIADFDEIISERFRQLEKI
KTIGSTYMAASGLNASTYDQVGRSHITALADYAMRLMEQMKHINEHSFNNFQMKIGLN
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GVVKKGKGEMTTYFLNGGPSS"
                                                                                             PRI 15-SEP-2000
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Wicker, R., Gascon Catalan, A., Cailleux, A.-F., Starenki, D.,

Stengel, D., Sarasin, A. and Suarez, H.G.

Direct Submission

Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite

genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer

CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICFIQLLIFPHSTLMLGIYASIFLLLLITVLICAVYSCGSLFPKALQRLSRSIVRSRA
HSTAVGIFSVLLVFTSAIANMFTCNHTPIRSCAARMLNLTPADITACHLQQLNYSLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAPLCEGTMPTCSFPEYFIGNMLLSLLASSVFLHISSIGKLAMIFVLGLIYLVLLLLG
PPATIFDNYDLLLGVHGLASSNETFDGLDCPAAGRVALKYMTPVILLVFALALYLHAQ
                                                                                                                                                                         Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6463)
Wicker, R., Catalan, A.G., Cailleux, A., Starenki, D., Stengel, D.,
Sarasin, A. and Suarez, H.G.
Cloning and expression of human adenylyl cyclase type VI in normal thyroid tissues
                                                                                 AF250226 6463 bp mRNA linear PRI 1
Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
AF250226
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AF250226
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Alignment Scores:

ORIGIN

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Homo sapiens chromosome 12 clone RP11-455122, WORKING DRAFT SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                    81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro 100
                                                                                                                                       874
                                                                                                                                                                                                                                                         695 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGC 754
                                                                                                                                                                                                       61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
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                                                                                                                                                                             1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly
                                                                                                                             21 GluArgAsnGlyGlnLysArgSerArgArgArgGlyThrArgAlaGlyGlyPheCysThr
                                                                                                                                                                  41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro
6463
99
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
 Length:
Matches:
Conservative:
                             Mismatches:
                                      Indels:
                                                Gaps:
                                                                    US-09-750-240-2 (1-104) x AF250226 (1-6463)
1.47e-26
545.00
97.06%
97.06%
95.61%
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                        995 GGCGGG 1000
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TITLE JOURNAL AUTHORS REFERENCE

REFERENCE

COMMENT

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Query Match:
                                                                                         source
                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
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9
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                                                         FEATURES
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rojuban, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, Y. Tangerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tang, H., Usmarisa, A., Tamerisa, A., Tamerisa, K., Wasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, G., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliamson, A., Wull, Wull, Wull, Wull, Wull, Y., Wu, Y., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (19-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 193283)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Apr 28, 2002 this sequence version replaced gi:15809061.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2133: contig of 2133 bp in length 2233: gap of unknown length 5400: contig of 3167 bp in length 5500: gap of unknown length 7889: contig of 2389 bp in length 7889: gap of unknown length 35565: contig of 23661 bp in length 35565: gap of unknown length 65717: gap of unknown length 65717: gap of unknown length 10448: contig of 29861 bp in length 10458: gap of unknown length 114586: contig of 41418 bp in length 146065: gap of unknown length 146065: gap of unknown length 146065: gap of unknown length 153283: contig of 47217 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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Worley, K.C.
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193283:
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TITLE
JOURNAL
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JOURNAL
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E 1 (bases I to 205248)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.K., Allen, C., Asbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Blange, K., Blankenburg, K., Bonnin, D., Bubay, C., Burch, P., Burkett, C., Brewn, M., Bryant, N.P., Bubay, C., Burch, P., Burkett, C., Byrd, N.C., Carren, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavazo, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., David, R., David, M., Davis, C., Coyle, M.D., Dathonne, S.R., David, R., David, M., Davis, C., Day, Carroll, L., Dederich, D.A., David, M., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Garbia, A., Garcia, A., Garner, T., Garza, N., Gill, R., Garbia, K., Harris, C., Harris, K., Hallins, B., K., Holloway, C., Hollins, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC117498 205248 bp DNA linear HTG 31-JUL-2002
Homo sapiens clone RP11-422021, *** SEQUENCING IN PROGRESS ***, 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                   715 others
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Mismatches:
Indels:
                                                                                                                                                  /clone="RP11-455122"
48888 c 46863 g 47544 t
                                                                                                                                                                                                                                                                                                 Length:
Matches:
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/db_xref="taxon:9606"
/chromosome="12"
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Location/Qualifiers
1. .193283
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AC117498.4 GI:22002346
HTG; HTGS_PHASE1.
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545.00
97.06%
97.06%
95.61%
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Best Local Similarity:
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Db 168819 GGCGGG 168814
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, Tx 77030, USA
On Jul 29, 2002 this sequence version replaced gi:21956504.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (10-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 205248)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 220255 bases at least 030
Consensus quality: 220255 bases at least 030
Consensus quality: 222408 bases at least 020
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Drafting Center Code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: RP11-422021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: HEAU
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2125:
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6733:
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2126
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COMMENT

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Db 168999 CCCGCTATATGAGCTGCCTCCGGGATGCAGCCACCCAGCCCCACCCTGCGGGCCC 168940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro 100
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                                                                                                                               gap of unknown length
contig of 3292 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 2331 bp in length
gap of unknown length
gap of unknown length
contig of 5888 bp in length
gap of unknown length
contig of 4730 bp in length
gap of unknown length
gap of unknown length
contig of 13851 bp in length
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of 14471 bp in length
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                                                                                 unknown length
of 2817 bp in length
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115533: contig of 17467 bp in
115633: gap of unknown length
139873: contig of 24240 bp in
139973: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown length
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Conservative:
Mismatches:
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/organism="Homo sapiens"
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us-09-750-240-2.rge

DEFINITION

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS

JOURNAL

COMMENT

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                    AC02557 171945 bp DNA linear HTG 07-JUL-2000 BOME Sapiens chromosome 12 clone RP11-579D7, WORKING DRAFT SEQUENCE, 17 unordered pieces.
                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MD 61108, USA
On Apr 27, 2000 this sequence version replaced gi:7574970.
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 171945) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                 Apr 27, 2000 this sequence version replaced gi:7574970
                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
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1962: gap of unknown length
3736: contig of 1774 bp in length
86925: contig of 1889 bp in length
7025: gap of unknown length
11773: contig of 4748 bp in length
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of 7165 bp in length
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AC02557.4 GI:7657832
HTG: HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
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RESULT 11
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81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu--
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1202 c 1257 g
                                                       97 ThrThrThrProAlaGlyPro 103
                                                                            428 GGGGCAGCTGGAGGTGGCCCT 448
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Sequence 1 from patent
129958
I29958.1 GI:1820749
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83.18$
82.89$
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SOURCE
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JOURNAL
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AR106659
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4046 bp mRNA linear MAM 27-APR-1993

Canis familiaris adenylyl cyclase type VI mRNA sequence.

M94968.1

M94968.1

GI:163896

adenylyl cyclase type VI.

Canis familiaris cardiac muscle cDNA to mRNA.

SM Canis familiaris

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

E (bases I to 4046)

Skatsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Halnon,N.J.,

HOMCY,C.J. and Ishikawa,Y.

Cloning and characterization of a sixth adenylyl cyclase isoform:
81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
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                                                                                     61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys
                                                                                                                                                                                                                                                                                                                                                                                          cyclase family
Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)
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Conservative:
Mismatches:
Indels:
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1. .4046
/organism="Canis familiaris"
/db_xref="taxon:9615"
/tissue_type="cardiac muscle"
a 1206 c 1254 g 843 t
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Matches:
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AR106659
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Ishikawa,Y.
Cloning and characterization of a c
Patent: US 5578481-A 1 26-NOV-1996;
Location/Qualifiers
                                                                          4046 bp
patent US 5578481.
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Search completed: March 1, 2003, 11:05:22
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Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.
M96160
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Premont, Kr., Chen, J., Ma, H. W., Ponnapalli, M. and Iyengar, R.
Two members of a widely expressed subfamily of hormone-stimulated
adenylyl cyclases
Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992)
93028552
1409703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenylate cyclase; adenylyl cyclase type VI.
Rattus norvegicus (strain Sprague-Dawley) adult liver, kidney,
heart conto to mRNA.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                   Multiple mechanisms underlying desensitization of the liver adenylyl cyclase system. Structure and cAMP regulation of liver
                                                                                                                                                                                                                                                                                                                                                                                                                 133 ACTCGGTGCCCCTGGCAGGATGAAGCCTTCATCAGGAGGGCTGGCCCGGGAAGGGGTGTG 292
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1 (bases 1 to 4131)
Tang, W.-J. and Gilman, A.G.
Soluble mammalian adenylyl cyclase and uses therefor
Patent: US 6107076-A 11 22-Aud-2000;
Location/Qualifiers
                                                                                                                                                                         Matches:
Conservative:
Mismatches:
Indels:

    .4131
    /organism="Rattus norvegicus"

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                                                                                    /organism="unknown"
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Premont, R.T.
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CHLRQLNYSTAUGYPTATTSONGASSNEFFDGLLGRSCHAPPIT
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LARERRNDELYYGSCECVAVWFASIANFSEYVELENNNEGYECLRLINEIIADFDEI
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7
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2
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Matches:
Conservative:
Mismatches:
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/product="adenylyl cyc
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                                                                                               14. _3556
/EC_number="4.6.1.1"
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                      OM protein – nucleic search, using frame_plus_p2n model
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Maximum Match 1008
Listing first 45 summaries
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7.0
7.0
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Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext :
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

11. Score Match 12. Score Match 13. Score Match 14. Score Match 15. Set 99.6 16. 545 99.6 17. 472.5 18. 99.5 18. 99.5 19. 94.16.5 19. 94.16.5 19. 94.16.5 19. 94.16.5 19. 94.16.5 19. 90.5 19. 90.5 19. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10. 90.5 10. 10.9 10.

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241 GAACTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAAGACAACGACACCG 300
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                                                                                                                                                         AAV23246;
                                          101
                                                                                                  RESULT 2
                                                                                                                AAV23246
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                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present cDNA sequence encodes human partial cardiac adenylcyclase VI (ACVI) isoform which is used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
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                                                                                                                                                                                                                                                                                                                                        Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluArgAsnGlyGlnLysArgSerArgArgArgClyThrArgAlaGlyGlyPheCysThr 40
                                      /product= "Human partial cardiac ACVI isoform #1"
/transl_except= (pos:229..231, aa:Xaa)
/transl_except= a n unknown amino acid; CDS does not include stop codon"
/EC_number= "4.6.1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             generating a third beta-ASP transgene, used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 114; 153pp; English
  Socation/Qualifiers
                                                                                                                                                                                     2000WO-US35411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76e-36
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                                                                                                                                                                                                                                                                                                WPI; 2001-418260,
P-PSDB; AAE04308
                                                                                                                             WO200148164-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                     26-DEC-2000;
                                                                                                                                                                                                                 27-DEC-1999;
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                                                                                                                                                                                                                                                                      Hammond HK,
                                                                                                                                                         05-JUL-2001
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 Key
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Pred

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The present sequence encodes human adenylylcyclase isoform VI (AC-VI) from the present invention. The present invention describes a recombinant replication-defective viral particle (I) comprising a gene encoding a beta-adrenergic signalling particle (I) comprising a gene encoding a beta-ASP) operably linked to a promoter. Also described are: (1) a recombinant pro-viral plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably collinked to a promoter and further comprising a replication-defective viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3) an isolated polynucleotide comprising a sequence encoding a human isolated polynucleotide comprising a sequence which hybridises at high stringency to (3); and (6) a vector comprising the polynucleotide of (3); and (6) a vector filtered adenovirus particle preparation. (I) is used to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; adenylylcyclase VI; AC-VI; beta-adrenergic signalling protein;
transgene; gene therapy; congestive heart failure; cardiac function;
adenovirus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vectors containing transgene(s) encoding beta-adrenergic signalling proteins - useful for gene therapy of congestive heart failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "adenylylcyclase isoform VI"
/transl_except= (pos:229..231,aa:Xaa)
/transl_except= (pos:315..317,aa:Xaa)
/note= "no stop codon given; Xaa = unknown"
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/note= "n indicates a gap of about 0.5 kb"
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                                                                                                                                                                                                                                                                                                                                   17-JUL-1998 (first entry)
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                                                             301 GCGGGACCGCTG 312
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P-PSDB; AAW53345.
AlaGlyProLeu
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fallure;
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/EC_number= "4.6.1.1"
                                                                                                                                    40
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                                                                                              ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro
                                                                                                                                                                                                                ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys
                                                                                                                                    GluArgAsnGlyGlnLysArgSerArgArgArgGlyThrArgAlaGlyGlyPheCysThr
                                                                                                                                                                                                                                                                                                                                                                                                                            Human, cardiant, beta-adrenergic signalling protein, beta-ASP, myocardium; gene therapy, beta-adrenergic receptor; beta-AR; adenylylycyclase; admb synthetase, depeted adenylyl throase; adenylate cyclase; camb synthetase, Grprotein receptor Kinase; GRK, heart disease; congestive heart; cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.
         2127
104
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                                                                                                                                                                                                                                                                                                                                                                                                            Human cardiac adenylcyclase VI (ACVI) isoform #1 DNA.
          Length:
Matches:
Conservative:
Mismatches:
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                                                                           US-09-750-240-2 (1-104) x AAV23246 (1-2127)
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         1.86e-35
568.00
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19
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                                      Best Local Similarity:
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                            Percent Similarity:
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Alignment Scores:
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                                                Query Match:
           Pred. No.:
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Human; cardiant; beta-adrenergic signalling protein; beta-ASP; myocardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylabete cyclase; cAMP synthetrase; adenylabete cyclase; cAMP synthetrase; G-protein receptor kinase; GRK; heart disease; congestive heart failure; cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.
                                                                                                              enhancing
                                                                                                      The present invention relates to methods and compositions for enhancin cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylytcyclases (also referred as adenylcyclase, adenylate cyclase and CAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present DNA sequence encodes human cardiac adenylcyclase VI (ACVI) isoform which is used for generating a third beta-ASP transgene, used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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           Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
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                                                                                                                                                                                                                                                                                                                                       Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;
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Matches:
Conservative:
Mismatches:
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                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-750-240-2 (1-104) x AAD08563 (1-3549)
                                                                           122-129; 153pp;
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545.00
97.06%
97.06%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                       of the invention
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                                                                           Example 5;
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241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300
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                                                                                 RESULT 5
                                                                                              AAD08568
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                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signaling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase adenylate cyclase and for treating heart disease, especially in mammalian hearts and for treating heart disease, especially congestive heart failure. The present DNA sequence encodes human cardiac adenylcyclase VI (ACVI) isoform which is used for generating a fourth beta-ASP transgene, used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro 100
                                                              /product= "Human cardiac adenylcyclase VI isoform #2" /EC_number= "4.6.1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 134-140; 153pp; English.
                       Location/Qualifiers
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                                                                                                                                                                                                                                                   Gao M;
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 Homo sapiens.
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Human; cardiant; beta-adrenergic signalling protein; beta-ASP; myocardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylatyclase; adenylathe cyclase; cAMP synthetase; Geprotein receptor kinase; GKK; heart disease; congestive heart failure; cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present cDNA sequence encodes human modified cardiac adenylcyclase VI (ACVI) isoform which is used for generating a beta-ASP transgene, used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
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/product= "Human modified cardiac ACVI isoform"
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                                                                                                                    81
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                                                                                                                                                                                ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys
                                                                                                ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro
                                                                                                                                                                                                                                                                                                                                                                 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCCAGGCAAGGGCAAG
                                                                         \tt MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGlyMetSerTrpPheSerGlyLouterProLysValAspGluArgLysThrAlaTrpGlyMetSerTrpPheSerGlyMetSerTrpPheSerGlyMetSerTrpPheSerGlyMetSerTrpPheSerGlyMetSerTrpPheSerGlyMetSerTrpPheSerGlyMetSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTrpPheSerTr
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Gaps:
                                  US-09-750-240-2 (1-104) x AAD08568 (1-3582)
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P-PSDB; AAW30599.
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N-terminus and a relatively shorter C-terminus as it lacks the C2b cepion. hAG6 cDNA was initially isolated from a human heart cDNA library using an adenylyl cyclase PCR fragment as probe. It was used to design primers that were used in a PCR-based RACE to obtain the full-length cDNA sequence. The invention relates to the hAC6 gene, methods for the recombinant production of purified hAC6 and the proteins made by these methods, antibodies against hAC6, vectors, probes and host cells (especially HEK-293) transformed by genes encoding polypeptides having hAC6 activity, along with a clarapeutic uses for these various reagents. hAC6 can be used as a tool to screen for agonists and antagonists that stimulate/inhibit hAC6. Such compounds have therapeutic utility in treating diseases caused by abberrant activity of this enzyme, in treating diseases caused by aberrant activity of this enzyme, while the compounds have their peuting or and diseases whose symptoms can be ameliorated by stimulating or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProArgCysProTrpGlnAspAspAlaPhelleArgArgGlyGlyPro***LysGlyLys
                                                                                                                                                                                                                                                                                                                                                                          Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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131..3627
/*tag= a
                                                                                                                                                                                                                                                                                                                            inhibiting the activity of hAC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cardiac adenylyl cyclase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ42525 standard; DNA; 4046
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545.00
97.068
97.068
95.618
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Best Local Similarity:
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Type VI adenylyl cyclase coding sequence.
                      03-JAN-2001 (first entry)
AAA53923;
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                                                                                                                                                                                   A canine heart cDNA library was constructed in lambda gtl0 and was screened with a 970 bp Aatl-Hincil fragment from type I adenylyl cyclase CDNA probe (encodes the first cytoplasmic domain of adenylyl cyclase, which has significant homology to other previously known types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd. Positive colonies were subcloned into puclB and further subcloned on a sequenced bidirectionally. The 5.4 kb clone was used to rescreen the library and on averlapping clone contg. the 5' end of the gene was isolated. Together the two clones cover the complete canine cardiac adenylyl cyclase gene. The gene is suspected of being involved in the regulation of cardiac function and it is thought that decreased activity of adenylyl cyclase in the heart may be a major factor in the development of heart failure. Thus the adenylyl cyclase gene is useful to screen cpds. which stimulate the activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 ATGTCGTGGTTTAGTGGCCTCCTGGTCCCCAAAGTGGATGAACGGAAGACAGCCTGGGGT 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluargasnGlyGlnLysArgSerArgargArgGlyThrArgAlaGlyGlyPheCysThr
                                                                                                                               Purified DNA encoding cardiac adenylyl cyclase - useful to screen for cpds. which stimulate activity of the cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu------val
                                                                                                                                                                                                                                                                                                                                                                 Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;
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89
2
11
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                 Claim 1; Fig 2; 34pp; English.
                                                     (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                                                                                                              9.62e-28
472.50
85.05$
83.18$
           92EP-0117374.
                               91US-0793961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 GGGCAGCTGGAGGTGGCCCT
                                                                                                  WPI; 1993-168873/21.
                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                            P-PSDB; AAR37309
                                                                                                                                                                                                                                                                                                                                            the cyclase
          12-OCT-1992;
                               18-NOV-1991;
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                                                                           Ishikawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
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AAA53923
ID AAA5
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A recombination and party cyclass is described with wild type enzyme is much easier compared with wild type enzyme sond the enzyme is more stable than the wild type enzyme which allows easier screening of compounds that stimulate and inhibit Adenylyl cyclase activity. The recombinant adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimera of adenylyl cyclase (1 and C_2 domains linked covalently. The domains may be linked by a linker peptide. The recombinant adenylyl cyclase is useful for screening inhibitors and stimulators of adenylyl cyclase activity. Inhibitors of the enzyme are useful for treating cholera, pituitary tumors, heart failure, ischemia, endocrine disorders and cell necrosis. Stimulators of adenylyl cyclase activity provides and stimulators of adenylyl cyclase activity provides and cyclase activity inhibitors of the enzyme are useful for cyclase are useful for treating pseudohypoparathyroidism and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl cyclase, is activated by Gsalpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluargasnGlyGlnLysArgSerArgargArgGlyThrArgAlaGlyGlyBheCysThr 40
Adenylyl cyclase; type I; type II; recombinant; enzyme; cAMP; cyclic AMP; adenosine monophosphate; screening; stimulation; ineatment; cholera; pituitary tumour; heart failure; ischaemia; endocrine disorder; cell necrosis; pseudohypoparathyroidism; endocrine deficiency; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant Adenylyl cyclase is described which lacks
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Conservative:
Mismatches:
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14..3556
/*tag= a
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432.00
86.27%
79.41%
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                                                                                                                                                                                               Homo sapiens
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Length: Matches:

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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199120 to AB199112, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB19913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                       116 GAACGCAATGGACAGAAGCGCCCA---CGCCAGGCGACCCGAGCCCGTGGCTTCTGCGCG 172
                               CCCCGCTACATGAGCTGCCTCAAGAATGTGGAGCCACCCAGCCCCACTCCTGCAGCTCGC
                                                                                                                                                   GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                              SS.
                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                                                                                                                                                                                                                                                                                                                                               Mouse ischaemic condition related cDNA sequence SEQ ID NO:716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi Y, Nagata T,
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                                                                                                                                                                                                                                                                                                     ABI99680 standard; cDNA; 5841 BP
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P-PSDB; ABB57257.
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Alignment Scores:

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213 CCTCGCTACATGAGCTGCCTCAAGAATGCGGAGCCACCCAGCCCCACTCCTGCAGCTCAC 272
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                                                                                                                                            GluArgAsnGlyGlnLysArgSerArgArgArgGlyThrArgAlaGlyGlyPheCysThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa DNA for cellular proliferation protein #249.
                                                                                                                                                                                    ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; ds; prokaryotic cellular proliferation gene;
antibiotic; antibacterial; drug design.
  5841
81
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                        Conservative:
Mismatches:
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                                                                            US-09-750-240-2 (1-104) x ABI99680 (1-5841)
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2000US-206648P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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1.98e-24
432.00
85.29%
79.41%
75.79%
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P-PSDB; AAU36259.
                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                  101 AlaGly 102
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26-MAY-2000; 2
23-OCT-2000; 2
27-NOV-2000; 2
22-DEC-2000; 2
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Yamamoto RT,
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                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella comenuoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery compounds nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
format directly from MIPO at
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Seq ID No 7755; 511pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1584 GCGTGGGTGAGCGGG-----GCGCCCCGATCAGGTCGTCGAAGAACTCCTGGTGGCTCT 1531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgArgGly------
                         /*tag- c
/note- "Potential translation initiation codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding regulatory activator protein srmR - for macrolide biosynthesis to increase efficiency of antibiotic prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 MetSerCysLeuArgAspAla------GluProProSerPro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2312 BP; 342 A; 862 C; 782 G; 326 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2312
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 3-4; 22pp; English.
                                                                                                                                                                                                                                                                                                  91US-0736178.
                                                                                                                                                                                                                                          92EP-0306792
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                                                                                                                                                                                                                                                                                                                                                                                                                         Rao RN, Turner JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGlyGlu 21
                              22 ArgAsnGlyGlnLysArgSerArgArgArgGlyThrArgAlaGlyGlyPheCysThrPro
                                                                                                                                                                                                42 ArgTyrMetSerCysLeuArgAspAlaGluPro-ProSerProThrProAlaGlyProPr
                                                                                                                                                                                                                                                                                          61 oArgCysProTrpGlnAspAspAlaPheIleArgArgGly 74
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                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi K, Saito K, Ya
A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2622 BP; 616 A; 748 C; 694 G; 564 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 14768; 2537pp + CD ROM; English.
                                                                                                                                              Human cDNA sequence SEQ ID NO:14768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
AAH16074 standard; cDNA; 2622 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999; 99JP-0248036.
27-AuG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0241899.
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                                                                                                 (first entry)
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                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                          EP1074617-A2
                                                                                               26-JUN-2001
                                                                                                                                                                                                                                                                                                                                          07-FEB-2001
                                               AAH16074;
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Prepn. of recombinant gB and gD is described in WO88504587. The amino acid sequence and DNA sequence for gB 1 presented in AAP80914 and AAN80907 differ from that originally presented in Table 1 of International Publication No. WO 85/04587. The DNA sequence in Table 1 contains an error in that an additional nucleotide (G) is listed at position 607 which resulted in a shift in reading frame relative to AAN80907 from which this nucleotide has been deleted.
                                                                                                                             Sequence of Herpes simplex virus (HSV) glycoprotein B (gB) 2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine for treatment of herpes simplex virus - contains recombinant HSV glyco:proteins B and D \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3474 BP; 666 A; 1183 C; 1058 G; 567 T; 0 other;
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819 ACTITIGCAAGTGGGAGGAGGGG-----AGAAGGGGA 849
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                     Location/Qualifiers 309..3023
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                                                  AAN80908 standard; DNA; 3474 BP
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                                                                                                                                                                                                                                                                                                                                 87US-0079605.
86US-0921213.
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                                                                                                    (first entry)
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                                                                                                                                                                              Herpes simplex virus.
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Best Local Similarity:
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                                                                                                    09-MAR-1992
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                                                                         AAN80908;
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                                       AAN80908,
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Matches: Conservative: Mismatches: Indels:

242 92.50 48.65% 33.78% 16.23%

Similarity:

Query Match: Best Local Score:

Percent Similarity:

Alignment Scores:

Gaps:

JS-09-750-240-2 (1-104) x AAH16074 (1-2622)

Length:

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AAV10362;
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                                                                                                                                                                     ------ValAlaLeuGlyLeuArgAla-----ValAlaLeuGlyPheGlu 92
                          34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of Herpes simplex virus ICP4 used in the method of the invention as modulators of apoptosis. The methods and products can be used to identify compounds which modulate (stimulate or inhibit) apoptosis in cells. They can be used to immortalise cells for the study of these cells or for growing cells in large numbers for the productions of proteins. They can also be
                       ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgArgGlyThrArg
                                                                                                                     Pro-----ThrProAlaGlyProProArgCysProTrpGlnAspAspAlaPhelleArg
                                                                    35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of herpes simplex virus U(s)3 polypeptide · for developing products for modulating apoptosis in cells and for identifying compounds which act as stimulators or inhibitors of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus ICP4; HSV ICP4; modulator; apoptosis;
stimulation; inhibition; HSV infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           The nucleotide sequence of the Herpes simplex virus ICP4
                                                                                                                                                                                                                                                                93 AspThrGluVal -----ThrThrThrProAlaGlyProLeu 104
                                                                                                                                                                                                                                                                              228 AAAACGTCTCGGTCGTAGACCACCGCGCCCGGTA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "HSV ICP4 protein"
                                                                                                                                                                  73 Arg-----GlyGlyPro***LysGlyLys-----
US-09-750-240-2 (1-104) x AAN80908 (1-3474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Pages 60-63; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      AAV68520 standard; DNA; 4257 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpes simplex virus.
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P-PSDB; AAW80810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leopardi R,
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                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of herpes simplex virus ICP4 polypeptide – useful for, e.g.
blocking apoptosis in cells, production of proteins and gene therapy
                                                                                                                                                                                                                                                                                       52 ro-ProSerProThrProAlaGlyProProArgCys------ProTrpGlnAsp
                                                                                                                                                                                                                                                                                                                                     68 AspAlaPhelleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein number 4; ICP4; alpha-4; cell apoptosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  3014 GCG------GCGACGACGACGACAAACCCCCCACGGGGCCG 3052
                                                                                                                                                                                                                                                                                                                                                                                     88 AlaLeuGlyPheGluAspThrGluValThrThrThrProAlaGlyPro 103
                                        T; 0 other;
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/*tag= a
/product= "Infected cell protein"
                                                                                                   Conservative:
                                                                                                                                                                                       17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer----
                                                                                                                 Mismatches:
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                                                                            Length:
Matches:
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used for stimulating apoptosis in cells, with a HSV infection.
                                        C; 1663 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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                                        BP; 412 A; 1768
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                                                                                                                 Best Local Similarity:
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                                        Sequence 4257
                                                                                                     Percent Similarity:
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                                                                 Aliqnment Scores:
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Disclosure; Fig 2; 63pp; English.

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The herpes simplex virus (HSV) alpha-4 gene encodes infected cell protein number 4 (ICP4). Both the alpha-4 gene and ICP4 can be used to block cell apoptosis. Similarly the administration of an agent that inhibits ICP4 or the alpha-4 gene can induce apoptosis in HSV infected cells. This can be used for the immortalisation of cells, production of proteins, gene therapy, or inhibition of cell death induced in vivo. They can also be used for production of therapeutics comprising inhibitors of HSV ICP4 function, useful for treating HSV function.
                                                                                                                                                                                                                                                                                                                                      17 ThralaTrpGlyGluArgAsnGlyGlnLySArgSer-----ArgArg-ArgGl 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ro-ProSerProThrProAlaGlyProProArgCys------ProTrpGlnAsp 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 AlaLeuGlyPheGluAspThrGluValThrThrThrProAlaGlyPro 103
                                                                                                                                                   Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T; 0 other;
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Matches:
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Mismatches:
Indels:
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SX CCCCCCCXX
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                                                        STATE: CA
COUNTRY: USA
ZIP: 94304-IDE
COMPUTER READBLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,097
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NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22000-20567.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09008097
Patent No. 6306830
GENERAL INFORMATION:
APPLICANT: Hammond, H. Kirk
APPLICANT: Ping, Peipei
APPLICANT: Ping, Peipei
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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  FILING DATE:
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                                                                                                     CITY:
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-MODEL-frame+p2n.model -DEV-x1h
-Q-Cgn2_1/USPTO_spool/US09750240/runat_25022003_103942_24989/app_query.fasta_1.263
-Q-(qn2_1/USPTO_spool/US09750240/runat_25022003_103942_24989/app_query.fasta_1.263
-Q-(qn2_1/USPTO_spool/US09750240/runat_25022003_103942_24989/app_query.fasta_1.263
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=-pct -THR_MAX=100 -THR_NIN-0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM-ext +HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0975040_GCN_1_1_17_erunat_25022003_103942_24989 -NOPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0 -FGAPOP=6 -FGAPEXT=7
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Sequence 5, Appli
Sequence 1, Appli
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Patent No. 5212296
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724.872 Million cell updates/sec
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1 MSWFSGLLVPKVDERKTAWG.....RAVALGFEDTEVTTFAGPL 104
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                                                                                                                               ; Search time 44
                     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                   - nucleic search, using frame_plus_p2n model
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US-09-008-097-5
US-09-474-076-1
US-08-240-357-1
US-08-240-357-1
US-08-736-136-11
US-08-690-473-1
US-08-659-1
US-08-659-1
US-08-458-568A-11
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
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Maximum DB seq length: 200000000
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Patent No. 6306830
GENERAL INFORMATION:
APPLICANT: Hammond, H. Kirk
APPLICANT: Drig, Paul A.
APPLICANT: Ping, Peipel
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                        US-09-750-240-2 (1-104) x US-09-008-097-1 (1-314)
                                                                                                                                                                                             Length:
Matches:
TELECOMMUNICATION INFORMATION
                                                                                                                        NAME/KEY: Coding Sequence LOCATION: LOCATION: 1...312
CTHER INFORMATION:
US-09-008-097-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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568.00
100.00%
100.00%
         TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                LENCTH: 314 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                              TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-008-097-5
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APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5028-01-US
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Conservative:
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                             FastSEQ for Windows Version 2.0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,097
FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Dylan, Tyler M
REGISTRATION NUMBER: 22000-205f
REFERENCE/DOCKET NUMBER: 22000-205f
TELEFAN.
TELEFANCE 1650-491-5600
TEL
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OTHER INFORMATION:
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OPERATING SYSTEM: DOS
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STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
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US-09-474-076-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Cloning and Character-
TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: ADDRESSE: ALIAN M. GOrdon
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                             US-09-750-240-2 (1-104) x US-09-474-076-1 (1-4942)
                                                                                                                                                                                                                                                                                            Length:
Matches:
CURRENT APPLICATION NUMBER: US/09/474,076
CURRENT FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: PCT/US98/13694
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 08/086,550
PRIOR FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                           TYPE: DNA ORGANISM: human type VI adenylyl cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07793961A
; Patent No. 5334521
  GENERAL INFORMATION:
  APPLICANT: Yoshihiro Ishikawa

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                                                                                                                                                                                                                                                                                        6.66e-38
545.00
97.06%
97.06%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (145)...(3648)
US-09-474-076-1
                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AlaGly 102
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                                                                                                                                                              LENGTH: 4942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-793-961A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                              Pred. No.:
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368 GAGCTGGGGCTGCGGGCGGTGGCCCTGGGCTTCGAGGACACTGAGGCCATGTCAGCGGTT 427
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Patent No. 5578481
GENERAL INFORMATION:
APPLICANT: ISHIKAWA, YOSHIHIRO
TITLE OF INVENTION: Cloning and Characterization of
TITLE OF INVENTION: Cardiac Adenylyl Cyclase
NUMBER OF SEQUENCES:
CORRESPONDED: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-750-240-2 (1-104) x US-07-793-961A-1 (1-4046)
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Matches:
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COMPUTER: IBM PC AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCIT from DW4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/793,961A
FILING DATE: 19911118
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: GO-COO., Alan M.
REGISCHRATION NUMBER: 31,705
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 203 321 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: American Cyanamid Company
One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                       FURMATION CO. CLE. --
SEQUENCE CHARACTERISTICS:
LENGTH: 4046 base pairs listed
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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472.50
85.05%
83.18%
82.89%
                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity:
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TITLE OF INVENTION:
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US-07-736-178C-1/c
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                                            COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: ENDAP disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NORMER: US/08/240,357
FILING DATE: 10-MAY-1994
CLASSIFICATION NUMBER: 335
ATTORNEY/AGENT INFORMATION:
NAME: GORGON, Alan M.
REGISTRATION NUMBER: 30,637
FELECOMMUNICATION NUMBER: 31,705-01
TELECOMMUNICATION NUMBER: 31,705-01
TELEFANATION NUMBER: 31,324
TELEFANATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4046 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Patent No. 6107076
GENERAL INFORMATION:
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APPLICANT: Gilman, Alfred G.
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472.50
85.05%
83.18%
82.89%
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US-08-240-357-1
            New Jersey
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                                     07470-8426
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Best Local Similarity:
Query Match:
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                        USA
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293 GAGCTGGGGCTGCGTCAGTGGCCTTGGGTTTTGATGACACTGAGGTG---ACCACACCG 349
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                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: TBM PC compatible
CORPUTER: TBM PC compatible
CORPRANTE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,642
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Matches:
Conservative:
Mismatches:
Indels:
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                                    TITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America ZIP: 77210
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432.00
86.27%
79.41%
75.79%
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STRANDEDNESS: single
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                         Houston
                                                                                                                                                                                                                                         CITY: Housto
STATE: Texas
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us-09-750-240-2.rni

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2846 CCGCCGCCCTGGAGGCCTACTGCTCCCCGCGCGCGCGCGGCCGAGCTCACGGAC---CACC 2902
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      71 IleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAlaValAlaLeuGly 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 ro-ProSerProThrProAlaGlyProProArgCys------ProTrpGlnAsp 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 AspAlaPheIleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAlaVal
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                                                                                                                                                                                     APPLICANT: Leopardi, Rosario
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERRES SIMPLEX VIRUS ICP4 AS AN
TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
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NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERNCE/DOCKET NUMBER: ARCD:239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
FILING DATE: 26-JUL-1996
CLASSIFICATION: 435
                                                                                                      US-08-690-473-1; Sequence 1, Application US/08690473; Patent No. 5876623; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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91.50
42.86%
36.73%
16.05%
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Best Local Similarity:
Query Match:
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US-08-690-473-1
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                                                                                                                                                                                                                                                                                                                                                         CITY: STATE:
                                            1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ThrProAlaGlyProProArgCys---ProTrpGlnAspAspAlaPhe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 ---AlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgArgGly------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 MetSerCysLeuArgAspAla------GluProProSerPro------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 ThrArgAlaGlyGly---PheCysThrProArg-------
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36
8
8
38
38
                                                         APPLICANT: Rao, Ramachandra N
APPLICANT: Turner, Jan R
TITLE OF INVENTION: ACTIVATOR GENE FOR MACROLIDE
TITLE OF INVENTION: BIOSYNTHESIS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/736,178C
FILING DATE: 19910726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19910726
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONTRACT ROBER: 32089
REGISTRATION NUMBER: 32089
REERERNENCE/DOCKET NUMBER: X8144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEPHONE: 317-276-1294
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly And Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
Sequence 1, Application US/07736178C Patent No. 5514544
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THEM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 317-2/0-123-
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2312 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.8
94.00
36.678
30.008
16.498
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STRANDEDNESS: single
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LOCATION: 345..2312
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                                                                                                                                                                                                                                                                                         46285
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OB:
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Query Match:
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                                                             Sequence 1, Application US/09259821A

Sequence 1, Application US/09259821A

Patent No. 6210926

GENERAL INFORMATION:

APPLICANT: LEOPARIO, ROSARIO

APPLICANT: LEOPARIO, RENARD

TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS

FILE REFERENCE: ARCD: 317

CURRENT APPLICATION NUMBER: US/09/259,821A

CURRENT FILING DATE: 1999-03-01

PRIOR FILING DATE: 1996-07-26

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2786 ACCCCTGGGCGGCTGGCGGCGGCAGCCCCGGGGCCCAAGGCGGGGGGCGCGCGGGG 2845
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3014 GCG------GCGACGACGACGATAACCCCCCACCCCACGGGGCCG 3052
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Patent No. 6218103
GENERAL INFORMATION:
APPLICANT: Loopardi, Roasrio
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERBES SIMPLEX VIRUS US3 AND ICP4 AS
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 AlaLeuGlyPheGluAspThrGluValThrThrThrProAlaGlyPro 103
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States
ZIP: 77221
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: HERPES VIRUS, TYPE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             48.6
91.50
42.868
36.738
16.058
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Best Local Similarity:
Query Match:
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CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 4257
                                                     US-09-259-821A-1
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                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Sequence 11, Application US/08458568A
Patent No. 5821339
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2846 CGGCGCCTGGAGGCCTACTGCTCCCGCGCGCGTGGCCGAGCTCACGAC---CACC 2902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AspAlaPheIleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAlaVal 87
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                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                    SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,659
FILING DATE: CONCURTENTLY HEREWITH
CLASSIFICATION: 435
                                                                                                                                                                                                                  ARSB:519
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPRECT 5.1
PC-DOS/MS-DOS
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: ARSI
TELECOMMUNICATION INFORMATION:
TELEPRONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.6
91.50
42.86%
36.73%
16.05%
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Best Local Similarity:
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COUNTRY:
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1012 TGTCGAGGGCGTCCTCGTACACCGTGCCGTCCCGGTTGGCTATCGAGTTGACGA 953
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                                                                                                                                                                                                                                                                                                                                                   38 Phe-----CysThrProArgTyrMetSerCysLeuArg 48
                                                                                                                                                                                                                                                                                                                                                                                                                   49 AspalaGluProProSerProThrProAlaGlyPro---ProArgCys---ProTrpGln 66 ::: ||| |||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 GlyGluArgAsnGlyGlnLysArgSerArgArgArg-----GlyThrArgAlaGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
5212296-5/c
; Patent No. 5212296
; APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
; J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
; TEPPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1879
30
6
26
19
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Matches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
                                                                                                                                                                  44.448
37.048
15.708
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89.50
44.44%
37.04%
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Best Local Similarity:
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Best Local Similarity:
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                                            SEQ ID NO:16:
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APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH

;J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.

;TEPPERRAN, JAMES M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 AlaLeuGlyPheGluAspThrGluValThrThrThrProAlaGlyPro 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
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Matches:
Conservative:
Mismatches:
Indels:
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      CURKENT APPLICATION DATA

APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-JUNE-1995
GLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI-0029
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 11:
SCHORNER CARRACTERISTICS:
COURNER CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
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APPLICATION NUMBER: US/07/569,781
APPLICATION NUMBER: 05/07/569,781
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                            LENGTH: 12001 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 GGTAGCCTGGGGGCGAGGTGCTGGAGGACCGAGTAGGATCGAGAAAACGTCTCGGTCG 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GluLeuGlyLeuArgAla-----ValAlaLeuGlyPheGluAspThrGluVal--- 96
                                      49 AspalaGluProProSerProThrProAlaGlyPro---ProArgCys---ProTrpGln
                                                                                             AspAspAlaPhelleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 ThrProArgTyrMetSerCysLeuArgAspAlaGluProProSerPro----ThrPro
                                                                                                                                                                                                                             Fatent No. 5244792

Patent No. 5244792

APPLICANT: BURKE, RAE L.; PACHL, CAROL; VALENZUELA, PABLO D.T.

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT GLYOPROTEIN

B FROM HERPES SIMPLEX VIRUS

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 1920

FILING DATE: 20-SEP-1990

FILING DATE: 20-CGT-1986

FILING DATE: 20-CGT-1986

FILING DATE: 06-APR-1984

FILING DATE: 06-APR-1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-144-759-17/c; Sequence 17, Application US/09144759; Patent No. 6117639; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 Pro***LysGlyLys-----
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Best Local Similarity:
Query Match:
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977 GTT 975
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APPLICANT: Hoock, Thomas
APPLICANT: Germann, Ursula
APPLICANT: Germann, Ursula
APPLICANT: Kwong, Ann
TITLE OF INVENTION: EUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS
TITLE OF INVENTION: USEFUL FOR MEASURING PROTEASE ACTIVITY
FILE REFERENCE: VPI/98-08
CURRENT APPLICATION NUMBER: US/09/144,759
CURRENT FILE DATE: 1998-08-31
SUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1575 TGGCGGGATGGCATGACTCCCTCGAGGAACTTGGGCAGTTTGT 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1396 GTATATAAATGCGTAGCGTGTCGATGTAGTAGCTCTGGATCGCTTCGACTAGCT---GGG 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1455 GATCGAGAGCAGCT-TTGCGTAGAAGACGAGGCTCATTGAGTCGCCGCAGTGGCGGTTGA 1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 -----ArgLysThrAlaTrpGlyGlu
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                                                                                                                                                                                                                                                                                                                                            Description of Artificial Sequence:man-made artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1279 CGTTGTCCACCTTCATCGAGAACATTTGGCGGCAGAAATGCAGCAGGTCTT 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 ArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAlaValAlaLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2241
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Mismatches:
Indels:
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Matches:
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ne : 51 secs
                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1
87.00
38.46%
32.48%
15.26%
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COTHER INFORMATION:
US-09-144-759-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                              SEQ ID NO 17
LENGTH: 2241
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Job time :
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Sequence 608, App Sequence 1479, Ap Sequence 41, Appl

Title: Perfect score:

on:

Sequence:

Scoring table:

Total number

Searched:

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sequence 59, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 1, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 11718, A
Sequence 1718, Appl
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Sequence 1, Appli
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Sequence 1, Appli
Sequence 1050, Ap
Sequence 6321, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hamon, H. K.
APPLICANT: Hamon, H. K.
APPLICANT: Hamon, H. K.
APPLICANT: Port, P.
APPLICANT: Port, P.
APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION NUMBER: US 09/472,667
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ. ID NOS: 13
SOSTWARE FESTSED FOR WINDOWS VERSION 4.0
                                                                           US-09-882-2888-1

US-09-883-2888-1

US-09-833-381-1050

US-09-833-381-1050

US-09-796-692-6321

US-09-776-888-1483

US-09-917-800A-1479

US-09-917-800A-1479

US-09-917-800A-1479

US-09-917-800A-1479

US-10-004-717-59

US-10-004-717-59

US-10-004-717-57

US-10-004-717-57

US-10-004-917-70-10

US-09-965-703-9

US-09-965-703-9

US-09-965-703-9

US-09-965-703-7

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US-09-965-703-7
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US-09-815-242-7988
US-09-864-761-15194
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US-09-042-48BB-6
US-09-042-48BB-8
US-10-096-961-3
US-10-096-859-888-3
US-09-859-888-3
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US-09-815-242-7755
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US-09-894-844-113
US-09-712-363-64
US-09-954-531-124
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280
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Sequence 5, Appli
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Sequence 12, Appl
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1063.219 Million cell updates/sec
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                                                                                                                                                                                                                                                  570
1 MSWFSGLLVPKVDERKTAWG.....RAVALGFEDTEVTTPAGPL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
//cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
                                                                                                                                                61 Seconds
                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                    OM protein – nucleic search, using frame_plus_p2n model
                                                                                                                                              ; Search time
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US-09-750-240-5
US-09-750-240-10
US-09-750-240-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                            460893 segs, 311809382 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                            March 1, 2003, 11:05:29
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 2000000000
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70:
110:
113:
144:
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Database

Score

Result 8

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; ORGANISM: Homo sapiens
US-09-750-240-5
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Sequence 5, Application US/09750240

Patent No. US20020103147A1

GENERAL INFORMATION:

APPLICANT: Hammon, H. K.

APPLICANT: Hammon, P. N.

APPLICANT: Ping, P.

APPLICANT: Post, S. R.

TITLE OF INVENTION: FAILURE

FILE REFERENCE: 220002056723

CURRENT FILING DATE: 120010-10-12

FRICH REPERENCE: 220002056723

CURRENT FILING DATE: 1999-12-27

PRIOR PLICATION NUMBER: US 09/472,667

PRIOR FILING DATE: 1999-10-16

PRIOR FILING DATE: 1999-01-16

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16
                                                                                                                                                                                        314
104
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                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                    Gaps:
                 ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1
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Best Local Similarity:
Query Match:
DB:
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US-09-750-240-5
LENGTH: 314
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GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrTro 100
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GENERAL NO. USZUGZUIO1

APPLICANT: Hammon, H. K.

APPLICANT: Insel, P. A.

APPLICANT: Dost, S. R.

APPLICANT: Post, S. R.

APPLICANT: Post, S. R.

APPLICANT: GAO, M.

TITLE OF INVENTION: FAILURE

FILE REFERENCE: 220002056/32

CURRENT APPLICATION NUMBER: US/09/750,240

CURRENT APPLICATION NUMBER: US 09/472,667

PRIOR FILING DATE: 1999-12-27

PRIOR FILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: US 09/24,757

PRIOR APPLICATION NUMBER: US 09/90-05

PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: US 60/048,933

PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: US 08/708,661
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                                           Conservative:
Mismatches:
Indels:
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             Length:
Matches:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-750-240-10
Sequence 10, Application US/09750240
; Patent No. US20020103147A1
           4.03e-40
545.00
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97.06%
95.61%
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Best Local Similarity:
Query Match:
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Alignment Scores:
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Score:
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APPLICANT: TOMILIBON, James E.
APPLICANT: TOMILIBON, James E.
APPLICANT: TOMILIBON, James E.
TITLE OF INVENTION: CLORAGE
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5028-01-US
CURRENT APPLICATION NUMBER: US/10/201,000
CURRENT APPLICATION NUMBER: US/20/44,076
PRIOR FILING DATE: 1999-12-12
PRIOR PLILING DATE: 1999-12-12
PRIOR PLILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
SPIOR PAPLICATION NUMBER: 06/070,904
PRIOR FILING DATE: 1997-07-01
SPIOR APPLICATION NUMBER: 06/070,01
SPIOR APPLICATION NUMBER: 08/070,01
SPIOR APPLICATION NUMBER: 08/070,01
PRIOR FILING DATE: 1997-07-01
SPIOR APPLICATION NUMBER: 08/070,01
SPIOR PRIOR FILING DATE: 1997-07-01
SPIOR APPLICATION NUMBER: 08/070,01
SPIOR PRIOR FILING DATE: 1997-07-01
SPIOR APPLICATION NUMBER: 08/070,01
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Indels:
                             US-09-750-240-2 (1-104) x US-09-750-240-12 (1-3582)
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95.61%
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Best Local Similarity:
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APPLICANT: HINFORMATION:
APPLICANT: HINSEL, P. A.
APPLICANT: Ping, P.
APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: GAUGE 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT PILING DATE: 1999-12.27
PRIOR APPLICATION NUMBER: US 09/402,667
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR PILING DATE: 1998-09-05
PRIOR FILING DATE: 1999-09-05
PRIOR FILING DATE: 1999-09-05
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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: DENERAL INFORMATION:
; APPLICANT: Harmnon, H. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12
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    Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                     205 GAACGCAATGGGCAGAAGCGTTCGCGGGCGCCGTGGCATCTGCAGGTGCTTCTGCACG 264
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                                                                                                                                                                                                                                                                    Sequence 165, Application US/09933797
Sequence 165, Application US/09933797
GENERAL INFORMATION:
TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
TITLE OF INVENTION: Sinus Expressed Sequences
FILE REFERENCE: 9901-007-999
CURRENT APPLICATION NUMBER: US/09/933,797
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US/09/482,933
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1099-05/14
PRIOR FILING DATE: 1099-05/14
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 811
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 165
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358
62
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Mismatches:
Indels:
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Matches:
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338.50
83.54%
78.48%
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                                                                                                                                                                                               101 AlaGly 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
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Patent No. US20020102543A1

GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020102543A1e1 Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-12-01
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Mismatches:
Indels:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ohisen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: DACATYOLES
FILTE REFERENCE: ELITRA. 011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/205,727
PRIOR APPLICATION NUMBER: 60/205,727
PRIOR APPLICATION NUMBER: 60/205,931
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/259,308
                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7755, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 CCTCGCTACATGAGCTGCCTC 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212.50
85.11%
85.11%
37.28%
                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus US-09-728-445-487
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 487
LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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2786 ACCCCCTGGGCGGCTGGCGGCGGCAGCCCCCGGGGCCCAGCCCACACGGCGCGCCCCGCGG 2845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SmithKline Beecham
STREET: Two, New Horizons Court, Great West Road
CITY: Brentford
STATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 AlaLeuGlyPheGluAspThrGluValThrThrThrProAlaGlyPro 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SmithKline Beecham plc et al
TITLE OF INVENTION: No. US20030022321A1el compounds
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTE: COMPUTE: COMPUTE: COMPUTE: COMPUTE: COMPUTE: Diskette
COMPUTE: IBM Compatible
COMPUTE: IBM Compatible
COMPUTE: SASTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/071,338
FILING DATE: OB-Feb-2002
CLASSIFICATION EQUARAND
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ANDE: Valentine, J111 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1182
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Conservative:
Mismatches:
                                                                                                                                                                                              52 ro-ProSerProThrProAlaGlyProProArgCys----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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MOLECULE TYPE: Other

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-071-338-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10071338 Publication No. US20030022321A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 0181-9752000
TELEFAX: 0181-9756294
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
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Best Local Similari
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Publication No. US20020192822A1
| GENERAL INFORMATION:
| APPLICANT: LEOPARDI | ROSARIO |
| TITLE OF INVERTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS |
| FILE REPERENCE: ARCD:3170SC1 | US/09/825,288A |
| CURRENT APPLICATION NUMBER: US/09/825,288A |
| CURRENT APPLICATION NUMBER: 09/259,821 |
| PRIOR APPLICATION NUMBER: 09/259,821 |
| PRIOR APPLICATION NUMBER: 09/259,821 |
| PRIOR FILING DATE: 1999-03-01 |
| PRIOR FILING DATE: 1999-03-01 |
| PRIOR FILING DATE: 1996-07-26 |
| NUMBER OF SEQ ID NOS: 2 |
| SOSTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 TCTGCTGGTGGCCGATGCCGAGGTCGCCGAGGGTGT---CGGGATCGATCGCCTCCA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 GGCCGACCTGGGCCATCGCCTCGCGGGCCGCGCGCGCA---GGCGCCGACGGTCGATCC 341
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7755
LENGTH: 1533
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                                                                                                                                                             TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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36.73%
16.05%
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39.13%
16.49%
                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (1)...(1533)
US-09-815-242-7755
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Best Local Similarity:
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Query Match:
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886 AGTGGTGGG-------CTCGC---CGGAGTCCCGGGAGACCAGGACGTCCTTCATCA 839
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                                                                            54
     34
15 ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgArgGlyThrArg
                                                                          35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKline Beecham
STREET: Two, New Horlzons Court, Great West Road
CITY: Brentford
STATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SmithKline Beecham plc et al
TTLE OF INVENTION: No. U$20030022321Alel compounds
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: CULK.

COUNTRY: CUK
ZIP: TW8 9EP
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/071,338
FILING DATE: 08-Feb-2002
CLASSIFICATION: <URKNOWN>
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Matches:
Conservative:
                                                                                                                                                       -----GlyProPro-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Valentine, vill B
REGISTRATION NUMBER: «Unknown>
REGISTRATION ON NUMBER: P31731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-071-338-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 0181-9752000
TELEFAX: 0181-9756294
                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10071338 Publication No. US20030022321A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 7193 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     ProThrProAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: Other
                                                                                                                                                                                                                                                               778 AGATGTCCA 770
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Query Match:
                                                                                                                                                                                                                             ArgCysPro 64
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Pred. No.:
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15 ArgLysThralaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgArgGlyThrArg 34

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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
                                                                                                                                                                                                                                                                   Sequence 1050, Application US/0983381

Sequence 1050, Application US/0983381

Patent No. US20020132090A1

GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVERTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR APPLICATION NUMBER: 09/516,448

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1050
                                                                 5381
5274 CGGTGAAGCCCATGGGGCCGAACCAGTTCTCGAAGATGAAGCCGCCGCCGCGGGGACGCCC 5333
                                                                                                                       494 GAC-----GCGGCTGCCTGCTGGGGGTGTGAGCGAGAGGCTGAGCGCTGCCCCCCCTCGGC 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 GCATCCATTCCGCACCGCCCCCTCCTGGGGGCCTCGGAGGAGCCCCCGCGCTGTGCG 381
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                                                      52 ------ProProSerProThrProAlaGly-------ProProArgCysPro
                                35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer
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                                                                                                     -----GlyProPro----
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Mismatches:
Indels:
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Matches:
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                                                                                                     ProThrProAla------
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38.46%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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                                                SOFTWARE: Patentin Ver.
SEQ ID NO 1483
LENGTH: 16489
                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-868-1483
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FEATURE:
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LOCATION: (137)
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Best Local Similarity:
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LENGTH: 398
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
CURRENT APPLICATION NUMBER: US,09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR PULICATION NUMBER: 60/196,126
PRIOR PELICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-01
PRIOR PELICATION NUMBER: 60/200,545
PRIOR PELICATION NUMBER: 60/200,545
PRIOR PELICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-27
PRIOR PELICATION NUMBER: 60/200,779
PRIOR PELICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR PELICATION NUMBER: 60/200,999
PRIOR PELICATION NUMBER: 60/200,999
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-04
PRIOR PELING DATE: 2000-05-04
PRIOR PELING DATE: 2000-05-22
PRIOR PELING DATE: 2000-05-22
PRIOR PELING DATE: 2000-05-31
PRIOR PELING DATE: 2000-06-04
PRIOR PELING DATE: 2000-06-04
PRIOR PELING DATE: 2000-06-04
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-04
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-04
PRIOR PELING DATE: 2000-08-04
PRIOR PELING DATE: 2000-08-04
PRIOR PELING DATE: 2000-08-07
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Matches:
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Patent No. US20020168711A1
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US-09-796-692-6321
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Best Local Similarity:
Query Match:
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US-09-764-868-1483
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                                                                                                                                                                                                                                                                              36 Gly---GlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer
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Fatent No. US20020055627A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR PRILING DATE: 2000-03-08
PRIOR PILING DATE: 12000-03-08
PRIOR SED IN OWNER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR SED ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
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Length:
Matches:
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OTHER INFORMATION: n equals a,t,g, or c
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NAME/KEY: misc_feature
LOCATION: (138)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (139)
OTHER INFORMATION: n equals a,t,g,
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290 GACCGGCGGGAGGCGCTTTCCGACCCCCAACTCGCGCCGGTGAT-----CCCCGT 237
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                                                                                                                                                                                                                                                                                               13 AspGluArgLysThrAlaTrpGlyGlu-----ArgAsnGlyGlnLysArgSerArg 29
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; NAME/KEY: misc_feature
; LOCATION: (377)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (386)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (394)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-608
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314, App 17, App 19, App 19, App 10, App 10, App 4032, App 42, App 13121, App 63, App 14, App 14, App 15, App 16, App 17, App 18, App 18, App 19, App 10, App 10, App 11, App 11, App 12, App 13, App 14, App 16, App 17, App 18, App 18, App 19, App 10, App 11, App 11, App 11, App 11, App 11, App 11, App 12, App 13, App 14, App 16, App 17, App 18, App 18, App 19, App 19, App 10, App 11, Ap

Sequence Seq

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of

Total number

Searched:

Minimum DB seq Maximum DB seq

Title: Perfect score: Sequence:

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Scoring table:

1266, A

Sequence Sequence Sequence Sequence Sequence

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US-10-288-985-1

US-10-289-980-1

US-09-724-676-9445

US-09-724-676-9445

US-09-724-676-9445

US-10-300-757-11

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US-10-329-079-34

US-09-585-645-59

US-10-329-079-34

US-09-585-6458-59

US-10-329-079-34

US-09-940-3168-1

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US-10-329-079-38

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PCT-US02-37547-56
US-10-144-771-44214
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US-10-144-771-15901
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US-09-949-004-512
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 83, Application PC/TUS0236759 GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BECHA, Shanya D.
YUE, Henry
LEHR-MASON, Patricia M.
THANGAVELU, Kavitha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIETZEN, Kimberly J.
LEE, Soo Yeun
AZIMZAI, Yalda
WALIAAI, Yalda
WALIA, Narinder K.
WARREN, Bridget A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   DUGGAN, Brendan M.
YANG, Junming
GIETTEN
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MARQUIS, Joseph P.
LAL, Preeti G.
FORSYTHE, Ian J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KALLICK, Deborah A. GRIFFIN, Jennifer A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEE, Sally
EMERLING, Brooke M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHARE, Reena
BAUGHN, Mariah R.
GANDHI, Ameena R.
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ELLIOTT, Vicki S.
GORVAD, Ann E.
  KABLE, Amy E.
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Sequence 5921,
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Sequence 78,
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/cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                   OM protein - nucleic search, using frame_plus_p2n model
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US-10-320-330-13
PCT-USO2-39133-56
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US-11-288-965-6
US-110-289-980-6
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APPLICANT: BLAKE, Julie J.
APPLICANT: BLAKE, Julie J.
APPLICANT: APPLICANT: CHENG, Menjin
APPLICANT: GAO, Jing
TITLE OF INVENTY RECEPPORS AND MEMBRANE-ASSOCIATED PROTEINS
FILE REFERENCE: PF-1279 PCT
CURRENT APPLICATION NUMBER: DCT/USO2/36759
CURRENT FILING DATE: 2002-11-13
PRIOR PLILING DATE: 2001-11-13
PRIOR PLILING DATE: 2001-11-15
PRIOR PLILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2002-01-11
PRIOR FILING DATE: 2002-01-14
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Matches:
Conservative:
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; OTHER INFORMATION: Incyte ID No: 7506194CB1
PCT-US02-36759-83
HAFALIA, April J.A.
                                                                                        BHATIA, Umesh
BURRILL, John D.
BLAKE, Julie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5e-34
545.00
97.06%
97.06%
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                 ISON, Craig H.
JIN, Pei
                                                 JIANG, Xin
JACKSON, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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APPLICANT:
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APPLICANT: American Home Product Inc.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEP TITLE OF INVENTION: DISORDER
FILE REFERENCE: AMA101250L
CURRENT APPLICATION NUMBER: US/60/423,552
CURRENT FILING DATE: 2002-11-05
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                     21 GluargasnGlyGlnLysargSerargargGlyThrargalaGlyGlyPheCysThr 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5921, Application US/10144771
GENERAL INFORMATION:
APPLICAMT: VENTER, J. Craig
TITLE OF INVENTION: HOMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: CL001321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 5921
                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
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Mismatches:
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Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-5921
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                                                                                                                                                       LENGTH: 5826
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Indels:

Query Match:

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HAPLICANT: Hoerster, George J.
TITLE OF INVENTION: Cyclin D Polynucloetides, Polypeptides
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 0926
CURRENT PAPLICATION NUMBER: US/09/398,858
CURRENT PILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 60/101,551
PRIOR FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 1173
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APPLICANT: Tao, Yunin
APPLICANT: Tao, Yunin
APPLICANT: Gordon-Kamn, William J.
APPLICANT: Gregory, Carolyn A.
APPLICANT: Gregory, Carolyn A.
APPLICANT: McElver, John A.
APPLICANT: McElver, John A.
TITLE OF INVENTION: Gorge J.
TITLE OF INVENTION: and Methods of Use
TITLE OF INVENTION: and Methods of Use
CURRENT FILING DATE: 2002-12-16
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
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Mismatches:
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Matches:
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
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57.78%
46.67%
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US-09-398-858-13
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Best Local Similarity:
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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US-10-320-230-13
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GRNERAL INFORMATION:
APPLICANT: American Home Product Inc.
APPLICANT: American Home Product Inc.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRES TITLE OF INVENTION: DISORDER
FILE REFERENCE: AM101250L
CURRENT APPLICATION NUMBER: US/60/427,579
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 256
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                3092 GETCACCIGICA TETA TETACT CIGACCIA A CGAGC CCACCCA GCACA GCACA COLOR 3151
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                                                                                                               3032 GCCAGTACACGGTCAAAAAGGACAAGGAGGAAACAGAGGCCAACGAAAGCTCAGAGGCCA 3091
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Matches:
Conservative:
Mismatches:
Indels:
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                                         US-09-750-240-2 (1-104) x US-60-423-552-78 (1-4955)
        Gaps:
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APPLICANT: Tao, Yumin
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gregory, Carolyn A.
APPLICANT: MCElver, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09398858 GENERAL INFORMATION:
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48.65%
33.78%
16.23%
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CRGANISM: Homo sapiens
US-60-427-579-78
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Best Local Similarity:
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                                                                                                                                   28 SerArgArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeu
                                                                                                                                                                                                 48 ArgAspAlaGluProPro-----SerProThrProAlaGlyProProArgCys---
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APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gregory, Carolyn A.
APPLICANT: McElver, John A.
APPLICANT: McElver, John A.
APPLICANT: Hoerster, George J.
APPLICANT: Hodersky, Sheila E.
TITLE OF INVENTION: Cyclin D Polynucloetides, Polypeptides
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 092602
CURRENT APPLICATION NUMBER: US/10/348,110
CURRENT FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 2002-12-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGT: 1173
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Conservative:
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GENERAL INFORMATION:
APPLICANT: Lowe, Keith S.
APPLICANT: Tao, Yumin
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US-10-348-110-13
                 Percent Similarity:
Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
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LOCATION: (1)
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APPLICANT: LEE, Sally
APPLICANT: HARALIA, April J.A.
APPLICANT: HERALIA, April J.A.
APPLICANT: HRAN, Bao
APPLICANT: STRAN, Bao
APPLICANT: STRAN, Bao
APPLICANT: STRAN, Bao
APPLICANT: TEE, Soo Yeun
APPLICANT: HEE, Soo Yeun
APPLICANT: HO, Anne
APPLICANT: HO, Anne
APPLICANT: HO, Anne
APPLICANT: HO, Anne
APPLICANT: STRANG, Wentlin
APPLICANT: APPLICANTON WHERE: 2002-12-04
FILE REFERENCE: FF-1319 PCT
CURRENT FILING DATE: 2001-12-20
FRIOR PELING DATE: 2001-12-20
FRIOR PELING DATE: 2001-12-20
FRIOR PELING DATE: 2002-01-15
FRIOR PELING DATE: 2002-01-15
FRIOR PELING DATE: 2002-01-15
FRIOR APPLICATION NUMBER: US 60/356,216
FRIOR APPLICANTION NUMBER: US 60/356,216
FRIOR APPLICATION NUMBER: US 60/356,216
FRIOR APPLICANTION NUMBER: US 60/356,216
FRIOR APPLICANTIO
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OTHER INFORMATION: Incyte ID No: 7506414CB1
PCT-US02-39133-56; Sequence 56, Application PC/TUS0239133; GENERAL INFORMATION:
                                                                                            APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: GRIFFIN, Jennifer A
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: BERRIING, Brooke M.
APPLICANT: ELIIOTT, VICKI S.
APPLICANT: ELIIOTT, VICKI S.
APPLICANT: BARGUIS, JOSEPH P.
APPLICANT: BARGUIS, JOSEPH P.
APPLICANT: GORVAD, Ann E.
                                                                                                                                                                                                                                                                                                                                                                                                      YUE, Henry
LEE, Ernestine A.
BECHA, Shanya D.
TANG, Y. Tom
TRAN, Uyen K.
SWARNAKAR, Anita
LEE, Sally
ISON, Craig H.
HAFALIA, April J.A.
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ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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Mismatches:
Indels:
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Matches:
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APPLICANT: Barton, Barry
APPLICANT: Barton, Barry
APPLICANT: Barton, Barry
APPLICANT: Griffin, John Patrick
APPLICANT: Griffin, John Patrick
APPLICANT: Griffin, John Patrick
APPLICANT: Griffin, John Patrick
APPLICANT: Paradkar, Ashish Sudhakar
TITLE OF INVENTION: Novel Process
FILLE OF INVENTION: Novel Process
FILLE REPERENCE: P31733C3
CURRENT FILLICATION NUMBER: 09/632,540
PRIOR APPLICATION NUMBER: 09/632,540
PRIOR FILING DATE: 1998-08-01
PRIOR PILING DATE: 1998-08-11
PRIOR FILING DATE: 1997-10-05
PRIOR FILING DATE: 1997-10-05
PRIOR FILING DATE: 1997-10-05
PRIOR FILING DATE: 1997-02-04
NUMBER: OF SEQ ID NOS: 19
SEQ ID NO 6
                                                                                                                                ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506415CB1
PCT-US02-39133-57
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                                                                  TYPE: DNA
ORGANISM: Homo sapiens
SOFTWARE: PERL Program
SEQ ID NO 57
                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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                                           LENGTH: 5079
                                                                                                                FEATURE
                                                                                                                                                                                                                                               Pred. No.:
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CURRENT PELLING DATE: 2002-12-04

PRIOR PELLING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-20

PRIOR PELLING DATE: 2001-13-60/342,761

PRIOR PELLING DATE: 2002-01-15

PRIOR PELLING DATE: 2002-01-15

PRIOR PELLING DATE: 2002-02-06

PRIOR PELLING DATE: 2002-02-12

PRIOR PELLING DATE: 2002-02-12
                                                                                                                                                                                                                                                                                                                               3102 GGGCCACGCTGGCAACCCCCGGGGACCACAGAGGGCATCTTCATCTCCAAGGTGAG 3161
                                                                                                                                                                                                                                                                                                                                                                                                           1162 CCCCACGGGGGAGCCGGGCGGAGGTGCGTGTGGGGTTTGCGGCTGTTGGAGGT 3221
                                                              2937 CGTGCGGGATGCCACGCA-------CCAAGAAGCAGTCAGTGCCCTGCTCCG 2981
                                                                                                                                                     2982 GCCCTGCCTGGAGCTGTCGCTGCTGGTGCGGAGGGACCCGGCACCCCCGGGCCTACGGGA 3041
                                                                                                                                                                                                                                        -----TrpGlnAspAspAlaPhelleArgArgGly------GlyPro 76
                    ArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAsp 49
                                                                                                                                                                                                 ----ProProArgCysPro 64
                                                                                                            --ProSerProThr---
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                                                                                                         AlaGluPro-----
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SPRAGUE, William W.
LEE, Soo Yeun
KHARE, Reena
GANDHI, Ameena R.
GIETZEN, Kimberly J.
BHATIA, Umesh G.
BURRILL, John D.
BLAKE, Julie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRIFFIN, Jennifer A
RAMKUMAR, Jayalaxmi
EMERLING, Brooke M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: INCYTE GENOMICS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KABLE, Amy E.
ELLIOTT, Vicki S.
MARQUIS, Joseph P.
BAUGHN, Mariah R.
GORVAD, Ann E.
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                                                                                                                                                                                              -----ProAlaGly----
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LEE, Ernestine A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shanya D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANG, Y. Tom
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35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer
                                                                                     ----GlyProPro----
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89.50
49.21%
41.27%
15.70%
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                                                                                     ProThrProAla -----
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778 AGATGTCCA 770
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Best Local Similarity:
                                                                                                                                            62 ArgCysPro 64
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LENGTH: 7193
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                                                                                                                                                                                                                 US-10-288-985-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                        35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer
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                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-289-980-6/c

| Sequence 6, Application US/10289980
| GENERAL INFORMATION:
| APPLICANT: Anders, Cecilia
| APPLICANT: Barton, Barry
| APPLICANT: Barton, Barry
| APPLICANT: Barson, Susan
| APPLICANT: Barson, Susan
| APPLICANT: Paradkar, Ashish Sudhakar
| TITLE NE FERENCE: P3173102C2
| CURRENT APPLICATION NOWER: US/10/289,980
| CURRENT FILING DATE: 2002-11-07
| PRIOR PRIOR APPLICATION NUMBER: US/350,976
| PRIOR FILING DATE: 1999-07-09
| PRIOR APPLICATION NUMBER: 09/350,976
| PRIOR FILING DATE: 1998-07-09
| PRIOR FILING DATE: 1998-07-04
| PRIOR FILING DATE: 1998-02-04
| NUMBER: OF SEQ ID NOS: 19
| SEQ ID NO 6
| LEWATT NOS IN SECO FOR WINGOWS VETSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Streptomyces clavuligerus
US-10-289-980-6
                                                                                  345
89.50
49.218
41.278
15.708
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89.50
49.21%
41.27%
15.70%
           ; TYPE: DNA
; ORGANISM: S. Clavuligerus
US-10-288-985-6
                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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778 AGATGTCCA 770
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Best Local Similarity:
Query Match:
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                                                                    Alignment Scores:
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5334 AGTGGTGGG------CCTCGC---CGGAGTCCCGGGAGACCAGGACGTCCTTCATCA 5381
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Mismatches:
Indels:
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Sequence 1. Application US/10288985

GENERAL INFORMATION:
APPLICANT: Barton, Barry
APPLICANT: Griffin, John Patrick
APPLICANT: Griffin, John Patrick
APPLICANT: Jensen, Susan
APPLICANT: Mosher, Roy Henry
APPLICANT: Paradkar, Ashish Sudhakar
ITILE OF INVENTION: Novel Process
FILE REFERENCE: P317333
CURRENT APPLICATION NUMBER: US/10/288,985
CURRENT FILING DATE: 2002-11-06
PRIOR FILING DATE: 1999-08-04
PRIOR PLICATION NUMBER: 09/137,737
PRIOR PLICATION NUMBER: 09/137,737
PRIOR PLILNG DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF
FILE REFERENCE: EX02-04G-PC
CURRENT APPLICATION NUMBER: PCT/US03/01858
CURRENT FILING DATE: 2003-01-22
FRIOR APPLICATION NUMBER: US 10/056,790
PRIOR FILING DATE: 2002-01-23
PRIOR FILING DATE: 2001-07-18
PRIOR PLILNG DATE: 2001-07-18
PRIOR PLILNG DATE: 2001-07-18
PRIOR PLILNG DATE: 2001-07-18
PRIOR PLILNG DATE: 2001-07-18
PRIOR PLING DATE: 2001-07-18
PRIOR PLING DATE: 2001-07-18
PRIOR PLING DATE: 2001-07-18
PRIOR PLING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/217,487
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer
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Matches:
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Mismatches:
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                             APPLICANT: MIGGES, COCILIA
APPLICANT: Barton, Barry
APPLICANT: Griffin, John Patrick
APPLICANT: Grason, Susan
APPLICANT: Mosher, Roy Henry
APPLICANT: Mosher, Roy Henry
APPLICANT: Paradkar, Ashish Sudhakar
TITLE OF INVENTION: NOVel Compounds
TITLE OF INVENTION: NOVEL COMPOUNDS
TITLE OF INVENTION: NUMBER: US/10/289,980
CURRENT APPLICATION NUMBER: 10/214,519
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 09/350,976
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1998-02-04
PRIOR RAPELEATION NUMBER: GB 9702218.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6e+03
89.50
49.21%
41.27%
15.70%
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Best Local Similarity:
GENERAL INFORMATION:
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PCT-US03-01858-47/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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5178 ACCACGCACCTGCTCCTGAATGAGCTGCAGCGAGCTCCTGTCCATAGAGCCGGGCCG 5119
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5118 AGGCCGGGGTCGCCCGAGGCCGGGAGGGGCTGCTCTGCGGA---
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Mismatches:
Indels:
Gaps:
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Matches:
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US60/305,017
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
SOFTWARE: PALENTING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PALENTIN VETSION 3.2
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LOCATION: (34301)..(34301)
OTHER INFORMATION: n is a, c,
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OTHER INFORMATION: n is a, C
FEATURE:
NAME/KEY: misc_feature
LCCATION: (34285)..(34285)
OTHER INFORMATION: n is a, C
FEATURE:
NAME/KEY: misc_feature
LCCATION: (34297)..(34298)
OTHER INFORMATION: n is a, C
                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
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Conservative:
Mismatches:
Indels:
Gaps:
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FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
TYPE: DNA
ORANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (42)
COTHER INFORMATION: n is a.c.g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51)...(51)
COTHER INFORMATION: n is a.c.g, or t
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

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-MODEL_frame+_p2n.model -DEV-xlh
-MODEL_frame+_p2n.model -DEV-xlh
-MCOFG1_1/102F0C_spool/J059750240/runat_25022003_103941_24976/app_query.fasta_1.263
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-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-UNITS-bits -START-1 -END--1 - MATRIX-b100 -TRRANIC-1 - ALGE-LOCAL
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-USER-US09750240_@CGN_1_1_899_@runat_25022003_103941_24976 -NCPU-6 -ICPU-3
-NO.AMAP -LARGEOURRY -NGC_SCORES-0 -WAIT -LONGIAG -DEV_TTMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
                                                          March 1, 2003, 07:59:04 ; Search time 1708 Seconds
  (without alignments)
  986.142 Million cell updates/sec
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Xgapop 10.0 , Xgapext
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gb_estl:* em_esthum:* em_estin:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	8	mRNA linear EST 27-NOV-2001 MRNA sequence. ata; Vertebrata; Euteleostomi; ognathi; Muridae; Murinae; Mus. Furuno, M., Hanagaki, T., Hirozane, T., Imotani, K., Ishii
в ІБ		618 bp ml -length enriched, G431005N18 5', ml 2730 Chordata; Crania' Rodentia; Sciuro, T., Carninci, P., O,K., Hiraoka, T.,
y th Length D	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	66520 RIKEN full culus CDNA clone 66520 66520 66520 66520 ase mouse. musculus aryota; Metazoa; nalla; Eutheria; (bases 1 to 618) nura,T., Arakawa atsu,N., Hiramot
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US-09-750-240-2 (1-104) x BB866520 (1-618)
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//Lissue_type="colon"
//Lissue_type="colon"
//Cell_line=RCB-0549 Cle-H3"
//Cell_line=RCB-0610 Cell_line=RCB-0035 WEHI-3),
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//Cell_line=RCB-0559 K-I FI), (cell_line=RCB-1283 B16
//Cell_type=RCB-0459 Cell_s, cell_line=RCB-1283 B16
//Cell_type=Leydig cells, cell_line=CRL-2065 MLTC-1),
//Cell_type=Nullipotent stem cell, cell_line=CRL-2070 WEH;
//Cell_type=Laydig cells, cell_line=RCB-0544 WBT-2),
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//Cell_type=B cells, cell_line=CRL-1669 BCLI Clone 13.20-3B3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-resigns.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinaki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
Laboratoryy for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (Tree)
The Institute of Physical Archive (Tree)
The In
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/clone_lib="RIKEN full-length enriched, colon RCB-0549
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Sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB866451 RIKEN full-length enriched, colon RCB-0549 Cle-H3 cDNA Mus musculus CDNA clone G431005J18 5', mRNA sequence.
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Unpublished (2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Schences Center(SCS), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Enx: 81-45-503-9216
Email: genome-reségsc.riken.go.jp,
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URL:http://genome.gsc.riken.go.jp/
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'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                               GluargasnGlyGlnLysargSerargargargGlyThrargalaGlyGlyPheCysThr 40
1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthonorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon: 1 (bases 1 to 1011) (bases 1 to 1011) (bases 2 to 1011) (bases 3 to 1011) (bases 3 to 1011) (bases 4 to 1011) (bases 5 to 10
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AL212334.1 GI:7871153
AL212334.1 GI:7871153
SS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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C (bases 1 to 1011)

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freshwater pufferfish Tetraodon nigroviridis
      162F16 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="colon"
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,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                            /organism="Mus musculus"
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Cle-H3 cDNA"
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/lab_host="bH10B (Life Technologies)"
/lab_host="labrary is a subtracted library derived polylinker; site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from on the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.

TAG_SEQ=None found*

76 a 130 c 152 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP CDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 94-126, SC_rich&Low_complexity
DOLYA-NO.
                                           AW045174 11-8-ST 18-SEP-1999 UI-M-BH1-alh-a-03-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alh-a-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. I (bases 1 to 430)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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Genome Res. 6 (9), 791-806 (1996)
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mEST@mail.nih.gov
                                                                                                                                 AW045174.1 GI:5905703
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112.00
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Fax: 301 443 9890
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Mus musculus
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                602814927F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4937095 5', BG916212
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                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 941)
                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10870 row: f column: 08
                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Príscilla Furth
Ph.D.
                                                                                                                                                                                                                                                                               NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lb="NOI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH108"
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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1. .941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 697)
Anderson,O.D., Chao,S., Crossman,C., Dubcovsky,J., Echenique,V.,
Anderson,O.D., Chao,S., Crossman,C., Stamova,B., Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat genomes - Vernalized apex cDNA library from Triticum monococcum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific 800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ803437 697 LPD mRNA linear EST 30-JUL-2002 WHE2837_F07_K13ZS Triticum monococcum vernalized apex cDNA library friticum monococcum cDNA clone WHE2837_F07_K13, mRNA sequence.
                                                                                                                       351 CTGCGAGCCTGGAGCGTCCCTGGTCACCAGCATAGACACCCAAGGAGGCGTAGATATTCG 292
                                                                                                                                                                                                                                                  411 GTTTCTTGGCCTGATGGCCTGCCTGGGCACATGCATCGGCAGCCACCCGTGGAAGAGCGA 352
                                                          16 LysThralaTrpGlyGluArgAsnGlyGlnLysArg-----SerArgArgGlyThr 33
                                                                                                                                                                                     34 ArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProPro 53
                                                                                                                                                                                                                                                                                                            Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 GGCTTTCCCACCAAGCTTGCACGCATCACACGCTCCTGGCCCGTTGCGGGC 121
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/dev_stage="One month old plants"
/lab_host="E. coli XLOLR"
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/organism="Triticum monococcum"
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BQ803437.1 GI:22018406
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG065197 1259 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-054103.F, genomic survey sequence.
AG065197
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                             519 ACCACCGCGACGCCGCTTTCTTGGGGCTAGCCGTCGCGGCCAGGGCGGTGATCTGCTCG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           579 ccgrccagacrccagcccargccgaagcccrccaccgccacgrcragrcgrgcrgraag 520
                                                                                                                                                                                                                                                                                   78 sGly-LysGluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrT 98
                                                                                                                                                                                                                                         ArgLysThrAlaTrp-GlyGluArg-----AsnGlyGlnLysArgSerArgArgArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1259)
Lordyyman, A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                 697
40
3
43
41
5
                                                                                                                                                                                                                                                                                                                                32 yThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCys-
                                            Matches:
Conservative:
                                                                                           Mismatches:
                      Length:
                                                                                                                    Indels:
                                                                                                                                             Gaps:
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R.Site 1 : SacI
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                                                                                           Best Local Similarity:
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/clone="IMAGE:4850910"
/clone=lib="Will_MGC_48"
/clone_lib="Will_MGC_48"
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/lab_host="DH100 (phage-resistant)"
/lab_host="DH100 (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average lnsert size 1.8kb. Library constructed by Ling HONG in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library." I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG558370 278 bp mRNA linear EST 10-APR-2001
RHIZ2_66_E02.bl_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
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Sukaryota, Vilolplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 583 0210
Exa: 706 583 0210
Email: mmpratt@uga.edu
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Unpublished (2000)
Contact: Cordonnier-Pratt MM
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High quality sequence start: 4
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Best Local Similarity:
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Query Match:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 897)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapabs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1692 row: o column: 07

High quality sequence stop: 811.
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others
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Mismatches:
Indels:
                                                                                                                                      924 GT-----GCGCGCGCGGGCCGGGCCAAAGAG 955
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                                                        /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-054103.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                Location/Qualifiers
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E I (bases to 842)

NIH-MCG http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                       1. .278
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/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes: Vector: pBluescript II from Lambda Zap II: Site_l: Khol; Site_2: Rcorf; The library was made Ifrom poly-A RNA in the cloning vector lambda ZAP II. clones to be sequenced were prepared by mass excision."
a 126 c 66 g 45 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 GCGTGG-----AGAGGCAGGTGGAAGGGGAAAAGGGGTGCAGGCCCTGGCTG 223
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Conservative:
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Indels:
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/db_xref="taxon:9606"
/clone="IMAGE:4075829"
/clone_lib="NIH_MGC_56"
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High quality sequence stop: 218 POLYA=No.
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Location/Qualifiers
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DEFINITION
                                                                                                                                                                                                                                                                     Pred. No.:
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TITLE
JOURNAL
COMMENT
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BF696034
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KEYWORDS
SOURCE
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/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (gyccottogan; bite_2: SfiI (gyccattatggcc);
SfiI (gycocttaggcc); Site_2: SfiI (gyccattatggcc);
Double-stranded CDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCCGCATG-AT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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BQ716276
BQ716276
BQ716276.1 GI:21855173
EST.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13599 row: d column: 20
High quality sequence stop: 454.
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1 (Dases 1 to 1048)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 GlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSerPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 ThrProAlaGlyProProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGly
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/db_xref="taxon:9606"
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//lab_host="DHIODS"
//lab_h
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 CGGAAGGACCGCGCGCGCGCGCGCGCGCGCGGTTTGCCCCGGTACCCCGCC 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 LysargSerArgArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSer 45
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 others
                                /clone_lib="Lupski_sympathetic_trunk"
/sex="male"
                                                                                                    /tissue_type="sympathetic trunk"
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Matches:
Conservative:
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                                                                                                                                       /dev_stage="adult, 16 yr"
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/clone="IMAGE:6194275"
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/crganian="Mus musculus"
/strain="C57BL/6J"
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/clone="U1-M-C50P-bd-c-10-0-UI"
/clone="U1-M-C50P-bd-c-
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
                        DNA Sequencing by: Dr. M. Bertto Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resqen.com).

The following respectitive elements were found in this cDNA sequence: 201-248, >GC_rich#Low_complexity

Seq primer: M13 REVERSE.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                               Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, yale University School of Medicine The following repetitive elements were found in this CDNA sequence: 1-62,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE900861 645 bp mRNA linear EST 29-SEP-2000 601673832F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956958 5',
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                                                                                                       Email: mEST@mail.nih.gov
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/note="Organ: placenta; Vector: pOTB7; Site_1: Xho1; Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into BCORI/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 64).
II (bases 1 to 64).
INH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                   CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM833 row: o column: 07
High quality sequence stop: 584.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 ACAGAGACCTCCCTGTTCAAGGCCCCTGACAGCTGTCCCTGC------CCTTCTTCC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 GAAGGGACTGGGAGGGGAGAGAGAGAAGGAGGGAAGGATTTAGGATGGTAAAGTTAGGT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGlyGlu 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ArgArgGly 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 ProSerProThrProAlaGlyProProArgCysProTrpGlnAspAspAlaPhelleArg 72
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/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
/clone="IMAGE:3956958"
/clone_lib="NIH_MGC_21".
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43.00%
33.00%
17.11%
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Location/Qualifiers

//Corganisme*Zea mays"

//Cone_lib=1007 - RescueMu Grid H*

//dev_stage="adult"

//dev_stage=
                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 366)
Walbot,V.
                                                                                                                                                                                                                                                                     Maize genomic sequences found using engineered RescueMu transposon oppublished (2001)
Contact: Malbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                 303 GCAGGTAGG---TGCCGTCCACGTCATCGCGATGTCGTCGGCGCGCTCCGCGCAGG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 CTGCGCCGTTGCGGAACGCCGGGAGCTTCCCGGAACTCCGGGAAGCTCCCGGCCCCCCGCGG 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 ------PhelleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArg
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Query Match:
                                                                   Zea mays.
                                                                                            Zea mays
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TITLE
JOURNAL
COMMENT
                              KEYWORDS
SOURCE
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Search completed: March 1, 2003, 11:35:39 Job time : 1713 secs

us-09-750-240-3.rng

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February 28, 2003, 19:58:51; Search time 259.906 Seconds (without alignments) 15700.357 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqn-embl/Na2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/Na2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/Na2001A.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result		Query				
No.	Score	Match	re Match Length DB ID	DB	ID	Description
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1					
	1812	100.0	1812	22	AAD08562	Human partial card
7	1812			19	AAV23246	Human adenvlvlcvcl
٣	1808.4			22	AAD08563	Human cardiac aden
4	1763.4			22	AAD08567	Human cardiac aden
2	1763	97.3	4942	20	AAX00461	Human type VI aden
9	1657.8			22	AAD08568	Human modified car
7	1527.8			14	AAQ42525	Cardiac adenylyl c
80	1437.2			21	AAA53923	Type VI adenylyl c
σ	1431.8			24	AB199680	Mouse ischaemic co

26-DEC-2000; 2000WO-US35411.

WO200148164-A2

05-JUL-2001

99US-0472667.

27-DEC-1999;

Human type V adeny	Cardiac adenylyl c	Cardiac adenylyl c	Type V adenylyl cy	Human adenylyl and	Drosophila melanog	Adenylyl cyclase t	Human adenylyl and	Adenylyl cyclase C	Drosophila melanog	Human cDNA sequenc	Human secreted pro	Type III adenylyl			۲	~	adenylate	Human NS cDNA segu	Rat adenylyl cycla	Adenylyl cyclase t	Human adenylate cy	Human adenylate cy	Human polynucleoti	Drosophila melanog	Type IV adenylyl c	Human adenylyl and	Drosophila melanog	'n	Drosophila melanog	Human secreted pro	Murine adenylate c	Human type IX aden	Human nervous syst	Drosophila melanog	Human prostate exp	
w	AAQ95540	AAQ37543	AAA53922	AAD28058	ABL07501	AAA53918	AAD28061	AAA53926	ABL15355	AAH16647	AAD34078	AAA53920	AAA53925	AAC99124	AAA53924	AAD06820	AAD31191	ABL39754	AAT14528	AAA53919	AAS02694	AAD31190	ABL90026	ABL29627	AAA53921	AAD28057	ABL02755	ABN89298	ABL16645	AAF33100	AAT35209	AAX00463	ABA14228	ABL14977	ABV25672	
20	16	14	21	24	23	21	24	21	23	22	24	21	21	21	21	22	24	24	17	21	22	24	24	23	21	24	23	24	23	22	17	20	22	23	23	
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O.	884.6	83	28	199	445.8	436	404	393.2	62	339	37	35	20	13	311.2	0	5	298	286	286	C)	8	273.6	67	26	5	N	240.2	34	30	19	8	189	188.2	172	
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ALIGNMENTS

RESULT 1

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Human; cardiant; beta-adrenergic signalling protein; beta-ASP; myocardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylate cyclase; cAMP synthetase; Gaptyclase; cadenylatese; Gaptotein receptor kinase; GKK; heart disease; congestive heart failure; cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ss.
                                                                                                                                                                                                                                       /*tag= a /product= "Human partial cardiac ACVI isoform #2" /product= "CDS does not include start and stop codon" /EC_number= "4.6.1.1"
                                                                             Human partial cardiac adenylcyclase VI (ACVI) isoform #2 cDNA.
                                                                                                                                                                                                              Location/Qualifiers 1..1812
AAD08562 standard; cDNA; 1812 BP.
                                                    (first entry)
                                                                                                                                                                                     Homo sapiens
                                                    04-SEP-2001
                        AAD08562;
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Indels
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                                                                                                                                                   Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0
                                                                                                                                                             DB
                                                                          present invention relates to methods and
                                                                                                                                                             Score 1812; I
Pred. No. 0;
0; Mismatches
                                                               English
                                                              5; Page 115-119; 153pp;
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100.0%;
                                                                                                                                                                        Conservative
     CALIFORNIA
                                         polynucleotide
l for enhancing
               Σ
                         2001-418260/44
                                                                                                                                                             Query Match
Best Local Similarity
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               Gao
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661 1141 1021 1141 1321 721 1021 1081 1081 1201 1201 1261 1321 1381 1381 1441 1501 1561 661 781 841 901 961 196 1441 1501 1561 901 1621 1621 QQ Ω 셤 Qγ g g ò g οŽ ద δy g QQ g g 셤 ò Ω δý δŻ Qγ Qγ ΩĐ δ g Qγ g ò g ò q οy d δ g ö enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic signalling proteins (beta-ASP) which increase encoding gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and 6-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present cDNA sequence encodes human partial cardiac adenylcyclase VI (ACVI) isoform which is used for generating a third beta-ASP transgene, used in the exemplification 540 CCGCGCAGCCCCTCTGCGGGCCTCTGGTGCCCTGTGTTTTGTATACATCGCATACACG 120 180 CTCCTCCCCATCCGCATGCGGGCTGCCGTCCTCAGCGGCCTGGGGCCTCTCCACCTTGCAT 180 240 240 300 300 360 420 420 480 480 540 900 900 lynucleotide encoding a modified adenylylcyclase polypeptide or enhancing cardiac function in mammalian hearts, and for heart disease, especially congestive heart failure -Gaps 9 9 GTTAACGTGGTGCTGGCCATCCTGGCGGCAGTGCAGGTCGGGGGGGCGCTTTCGCAGCAGCA CTCCTCCCCATCCGCATGCGGGCTGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCAT TTGATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCC AATGTGCTGCTGTTCCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAG GTGTCTCAGCGCCAGGCCTTTCAGGAGCCCGCAGTTACATCCAGGCCCGGCTCCACCTG CAGCATGAGAATCGGCAGCAGGAGCGGCTGCTGTCGGTATTGCCCCAGCACGTTGCC CAGCATGAGAATCGGCAGCAGCAGCGGCTGCTGCTGTCGGTATTGCCCCCAGCACGTTGCC **ATGGAGATGAAAGACATCAACACAAAAAAAAAAGAAGACATGTTCCACAAGATCTACATA** CAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCA TCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGAC 1812; ö compositions for Length 301 301 361 361 421 421 481 541 541

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sequence which hybridises at high stringency to (3); and (6) a we comprising the polynuclectide of (3). (1) can be used to form a filtered adenovirus particle preparation. (1) is used to enhance cardiac function in mammals.
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Best Local Similarity 100.
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Similarity
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Human; cardiant; beta-adrenergic signalling protein; beta-AS mycoardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylylcyclase; adenylylate cyclase; cAMP synthetase; effortain receptor kinase; GRK; heart disease; congestive he cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene;
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Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
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Page 134-140; 153pp; English Claim 6;

The present invention relates to methods and compositions for enhancin cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylytcyclases (also referred as adenylcyclases adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present DNA sequence encodes human cardiac adenylcyclase VI (ACVI) isoform which is used for generating a four the teach and the exemplification the invention

BP; 686 A; 1037 C; 1068 G; 761 T; 0 other; Sequence 3552

ä 1115 1235 629 695 122 182 815 242 875 302 935 362 995 422 479 599 Gaps 62 GTCTCAGCGCCCAGGCCTTTCAGGAGCCCGCAGTTACATCCAGGCCCGGCTCCACCTGCA GCATGAGAATCGGCAGCAGCAGCTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCAT GCGCAGCCCCTCTGCGGGCCTCTGGTGTTCTTTGTATACATCGCATACACGCT CCTCCCCATCCGCATGCGGGCTGCCGTCCTCAGCGGCCTGGGGCCTCTCCCACCTTGCATTT GATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAA TGTGCTGCTGTTCCTCTGCACCACGTCATTAGCATCTGCACACACTATCCAGCAGAGGT 996 GCATGAGAATCGCCAGCAGCAGCGCTGCTGCTCGGTATTGCCCCAGCACGTTGCCAT TGTGTCAGGGCTGCCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGGAGATGGGGGT GGAGATGAAAGACATCAACACAAAAAAAAGAAGAC---ATGTTCCACAAGATCTACAT 480 ACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC 540 ATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCCGGTTTGA CAAGCTGCCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGGACTGTTACTACTG Score 1763.4; DB 22; Length 3552; Pred. No. 0; 0; Mismatches 21; Indels 3; Query Match 97.3%; Best Local Similarity 98.7%; Matches 1789; Conservative 936 ო 123 756 183 918 243 876 1296 63 303 363 423 9 099 ò 엄 ŏ g οy g q 원 q qq g a ò ò ò à οŽ οy Db Óγ g δý ò

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                                                TCGGGCCAACTCCATGGAAGGCCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCG
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N-terminus and a relatively shorter C-terminus as it lacks the C2b in the company of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newly isolated and purified human type VI adenylyl cyclase (hAC6) by/peptide - useful for identifying potential therapeutic agents that modulate hAC6 activity, and for the diagnosis of hAC6-associated diseases and disorders
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                               Human type VI adenylyl cyclase cDNA.
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                                               AAX00461 standard; cDNA; 4942 BP
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GGGCCAACTCCATGGAAGGGCTGATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCGGA 1921
                                                                                                                     AGAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACG
                                                                                                  GCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTG
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The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the mycoardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adennylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetaes) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present cDNA sequence encodes human modified cardiac adenylcyclase VI (KCVI) isoform which is used for generating a beta-ASP transgene, used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
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/product= "Human modified cardiac ACVI isoform"
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A canine heart cDNA library was constructed in lambda gt10 and was screened with a 970 bp AatI-HincII fragment from type I adenylyl cyclase cDNA probe (enrodes the first cytoplasmic domain of adenylyl cyclase, which has significant homology to other previously known types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd. Positive colonies were subcloned into pUC18 and further subcloned and sequenced bidirectionally. The 5.4 kb clone was used to rescreen the library and on averlapping clone contg. the 5' end of the gene was isolated. Together the two clones cover the complete canine cardiac adenylyl cyclase gene. The gene is suspected of being involved in the regulation of cardiac function and it is thought that decreased activity of adenylyl cyclase in the heart may be a major factor in the development of heart failure. Thus the adenylyl
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TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGGAGCTG
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cyclic AMP; adenosine monophosphate; screening; stimulation;
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                                                                                                                                                                                                                                                                                                                                                A recombinant Adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzyme which allows easier screening of compounds that stimulate and inhibit Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimera of adenylyl cyclase comprises a chimera may be linked by a linker peptide. The recombinant adenylyl cyclase is useful for screening inhibitors and stimulators of adenylyl cyclase activity. Inhibitors of the enzyme are useful for treating cholera, pitultary tumors, heart failure, ischaemia, endocrine disorders and cell necrosis. Stimulators of adenylyl cyclase are useful for treating pseudohypoparathyroidism and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl cyclase, is activated by Gsalpha
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  tumour; heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;
inhibition; treatment; cholera; pituitary tumour; heari
ischaemia; endocrine disorder; cell necrosis;
pseudohypoparathyroidism; endocrine deficiency; human;
                                                             Location/Qualifiers
14..3556
/*tag= a
/product= Type VI adenylyl cyclase
                                                                                                                                                                                                                                                                                                                             Disclosure; Columns 75-78; 73pp; English.
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method
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2127 ACTCCGCCCTGATACTCGGGATTTATGCCGGGATCTTCCTTTTGCTGCTGGTCACCGTGC
                                                                                           1742 ATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTC
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                                                                                                                         GCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTTG
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                                                                                                                                                                                                                 Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse ischaemic condition related cDNA sequence SEQ ID NO:716
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P-PSDB; ABB57257.
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condition related sequence
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           ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB5734) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence which are used in the exemplification of the present invention.
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                                                                                                                                                                            DB 24; Length 5841;
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                                                                                                                                                Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;
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ischaemic condition (e.g.
                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                            Score 1431.8;
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                                                                                                                                                                                          Pred. No.
                                                                                                                                                                            79.0%;
87.7%;
  useful for examining the
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Best Local Similarity 87.7
Matches 1588; Conservative
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brain;

human; hAC5; heart disease;

cyclase;

(first entry)

98WO-US13540. 97US-0886362. 97US-0070901.

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Newly isolated and purified human type V adenylyl cyclase (hAC5) elypeptide - useful for identifying potential therapeutic agents that modulate hAC5 activity, and for the diagnosis of hAC5-associated diseases and disorders
                                  Human type V adenylyl cyclase coding sequence
                                                                                                                                                                        (CORT-) COR THERAPEUTICS INC
                                                Type V adenylyl cyclase
therapy; diagnosis; ds
                                                                                                                                                                                                        WPI; 1999-106048/09.
                                                                                                                                                                                                                  P-PSDB; AAW30600
                                                                                                                                                                                         Tomlinson JA;
                                                                            Homo sapiens
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AAX00462;
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        GGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGA 1141
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                                           GCCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCC 1021
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                                                                                                    TGGGCGCCAGCCAGAAACGGAAAGAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTC
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                                  GCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAG
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This sequence encodes the human type V adenylyl cyclase (hAC5) of the invention. hAC5 has a similar putative structure to other adenylyl cyclase isoforms but, like type VI, is distinguishable in that it has a caracter as a similar type VI, is distinguishable in that it has a larger N-terminus and a relatively shorter C-terminus as it lacks the correction. The hAC5 polypeptides are useful in assays that screen for potential therapeutic agents, which modulate hAC5 activity. These collopeptides are also useful in assays for the diagnosis of diseases and disorders. Agonists of hAC5 are useful control agents in such assays, and they may have useful effects in vivo for treating disease. Antibodies acting as (ant)agonists have diagnostic and therapeutic effects, and are useful in immunoassays for hAC5. (Ant)agonists are particularly useful in treating diseases caused by abnormal hAC5 activity (e.g. In the heart and brain), and in diseases, which are alleviated by modulating hAC5 activity. The oligonuclectides are useful in methods that inhibit or regulate hAC5 enables the development of tissue-specific and selective and society apparagonists have in treating particular human diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 895; DB 20;
Pred. No. 5.7e-229;
0; Mismatches 525;
Claim 3; Fig 1a-h; 40pp; English.
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Matches 1277; Conservative
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AAX00462 standard; DNA; 4523 BP

RESULT 10
AAX00462
ID AAX00
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1310	Db 2360 TCCTGACCTTCAGGGAGCCTGACTTP Qy 1370 TCGGAGCCTACGTTGCCTGGCCTG	rereece ACACTCC	2480	2540	QY 1550 AACGTCTGTCCCGCAGCATTGTCCGC	Qy 1610 CCGTCCTGCTTGTGTTACTTCTGCC	Qy 1670 TACGGACCTGTGCAGCCCGGATGCTG	Qy 1730 TGCAGCAGCTCAATTACTCT	Oy 1784 IGCCCACCIGCAGCITICCIGAGGIG	RESULT 11 AAQ95540 ID AAQ95540 standard; DNA; 4356 BP	XX XX AAQ95540; AC XX XX DT 31-JAN-1996 (first entry)	XX DE Cardiac adenylyl cyclase gene. XX XX	Homo sapiens.	FT CDS 1483702 FT CDS 1483702 FT X /*tag= a	_	PD 21-MAR-1995. XX PF 02-JUL-1992; 92TW-0105242.	XX PR 12-JUN-1992; 92US-0899068. XX DAMPY) AMERICAN CVANANTH CO	WPI; 1995-214006/28. P-PSDB; AAR78519.	AA PT Cardiac adenylyl cyclase and co PT sequences XX	PS Claim 1; Fig 2; 45pp; Chinese.
Db 1226 CCATCGCCCTGCGCACCAACGCCCAGGACCAGTTCCTGCTGAAGCAGCTTGTCTCCAATG 1285 Qy 245 TGCTGCTGTTCCTCTGCACCAACGTCATTAGCATCTGCACACACA	Db 1286 TTCTCATTTCTCCTGCACCAACATCGTGGGTGTCTGCACCCACTATCCGGCTGAGGTCT 1345 Oy 305 CTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGC 364	1346 CCCAGAGACGCTTTCCAGGAGACCCGAGAGTGCATCCAGGCGCGCTCCACTCGCAGC	UY 353 ATGAGAATCGGCAGCAGGACGGCTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGG 424	OY 425 AGATGAAAGAAGACATCAACAAAAAAGAGACATGTTCCACAAGATCTACATAC 481	QY 482 AGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCAT 541		Oy 602 AGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTG 661	QY 662 TGTCAGGGCTGCCGGAGGCCCGGCCGACCATGCCCACTGCTGTGGAGATGGGGGTAG 721		QY 782 TGGGCATCCACAGCGGGGGGGGTGCACTGCGTCCTTGGCTTGCGAAATGGCAGTTCG 841	QY 842 ATGTGTGGTCCAATGATGTGACCCTGGCCAACCACGGAAGCAGGAAGCCGGGCTGGCC 901 I	Qy 902 GCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAG 961 	962 GCCGTGGCGAAGCGCTAACGTCAAGGACACCACATGGAGCTTTCCTCATC	2006	2066 TGCGCTGCACCCAGAAGCGGAAAGAAGAAGAGGCCATGATCGCCAAGATGAACCGCCAGA	<pre>UV 1082 GGGCCAACTCCATGGAAGGCTGATGCGTTCCTGATCGTGCCTTCTCC 1137</pre>	Qy 1138 CGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGCCATTGATGATGATGCAGCA 1189 Db 2186 ACCTGGGTGGCAACCAGGTGTCCAAGGAGATGAAGGGATTGAAGGCGATTGAAGACCA 2242	124	1250 GCCGTGCCATCGATGCCCGCAGCATTGATCAGCAGCGAAGGACCATGTGCGCCGGTTTT 130	Db 2300 GCCGTGCCATTGACGCCAGGAGCATTGATAGGCTTCGGTCTGAGCACGTCCGCAAGTTCC 2359

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AGGGAGCCTGACTTAGAGAAGAAGTACTCCAAGCAGGTAGACGACCAT 2419
                                       CGCAGCATTGTCCGCTCACGGGACATAGCACCGCAGTTGGCATCTTT 1609
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                                                                                                                                        SIGITIACTICICCATICCCAACAIGTICACCIGIAACCACCCCCA 1669
                                                                                                                                                                                                                         cyclase and corresp. DNA - having specified
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                                                 TGGGCGCCAGCCAGAAACGGAAAAGGGGAAAGGCATGCTGGCCAAGCTGCAGCGGGACTC 1081
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   GCCGTGGTGGCAAGCGCGAACGCGTACCTCAAGGAGCACACATTGAGACTTTCCTCATCC
                1961 ACCTAGGAGGCAACCAGGTGTCCAAGGAGATGAAGCGCATGGGCTTCGAAGACCCCAAGG
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  effector enzyme cardiac adenylyl
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                                                                                  15;
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                                  BP; 836 A; 1372 C; 1373 G; 775 T; 0 other;
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                                                       Score 884.6; DB 16;
Pred. No. 3.4e-226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Left ventricular tissue of canine heart was used as a source of mRNA. A cDNA library was prepd. in lambda gt10 phage. A 970 bp Aat-HincII fragment from type I adenyly1 cyclase cDNA was used as probe. The clones isolated were used to obtain CDNA encoding CACV. This probe may also be used to screen a human cardiac cDNA library to obtain the cDNA encoding human CACV. CACV, its analogues and antibodies are useful in thraspy or diagnostic assays, e.g. in modifying and determining cardiac function. A decrease in CACV content of the heart contributes to impaired cAMP prodn. and in heart failure. The CACV can also be used to screen for cpds. which stimulate or inhibit
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                                                        Location/Qualifiers
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                      GCCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACCATTGAGACTTTCCTCATCC 1021
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CCGTGCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTC 1555
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                                          TGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGGA
                                                                              CSTCGGCGGCCACTCAGCCTGGGCGACGAGCAGGCTTCTGCGGCACGCCCTGGCCCA
                TGGTATTTGTCTCCGTGATCTATTCCTGCGTGAAGCTCTTCCCGGGCCCCGCTCCAGAGCC
                                TGTCCCGCAGCATTGTCCGCTCACGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCC
                                                                                                                                        AGCTCAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A recombinant Adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzyme which
                                                                                                     Adenylyl cyclase; type I; type II; recombinant; enzyme; cAMP; cyclic AMP; adenosine monophosphate; screening; stimulation; inhibition; treatment; cholera; pituitary tumour; heart failure; ischaemia; endocrine disorder; cell necrosis; pseudohypoparathyroidism; endocrine deficiency; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                    3..3329 /*
/*tag= a
/product= Type V adenylyl cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Columns 65-70; 73pp; English.
                                                                                                                                                                                                                                                                                         Type V adenylyl cyclase coding sequence.
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                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                Length 3924;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                 Sequence 3924 BP; 860 A; 1103 C; 1110 G; 851 T; 0 other;
                                                                                                                                                                                                                                                                                           Score 858.2; DB 21;
Pred. No. 3.8e-219;
0; Mismatches 548;
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                                                                                                                                                                                                                                                                                                                  Best Local Similarity 68.6
Matches 1254; Conservative
                                                                                                                                                                                                          endocrine deficiencies.
                                                                                                                                                                                                                                                                                                Query Match
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Human; adenylyl and guanylyl cyclase; ADGUC-2; cardiovascular disorder; analyse angina peetoris; mycoardial infarction; vision disorder; keratitis; iritis; cataract; neurological disorder; epilepsy; Alzheimer's disease; Pick's disease; stroke; mental disorder; mood and anxiety disorder; reproductive disorder; infartility; endometriosis; impotence; asthma; smooth muscle disorder; migraine; bacterial infection; gene therapy; transgenic animal; vaccine; enzyme; ss.

/*tag= a /product= "Human ADGUC-2 protein"

/*tag=

WO200202757-A2

10-JAN-2002

Location/Qualifiers

Homo sapiens

Human adenylyl and guanylyl cyclase (ADGUC)-2 cDNA.

(first entry)

22-APR-2002

AAD28058;

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                  GCCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCC
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                                                             GCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAG
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Yue H, Yang Elliott VS;

Lee EA, Yu Tang YT,

Lu DAM, Walia NK,

ŗ Ding L, Yao MG,

Tribouley C, Thornton M,

(INCY-) INCYTE GENOMICS INC.

2000US-223545P. 2000US-229876P. 2000US-234838P.

04-AUG-2000; 31-AUG-2000; 22-SEP-2000; 29-SEP-2000;

29-JUN-2000;

2001WO-US20491

26-JUN-2001;

2000US-236483P

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The invention relates to human adenylyl and guanylyl cyclases (ADGUC)
preferably ADGUC1-ADGUC5 and nucleic acid molecules encoding such
polypeptides. ADGUC sequences are useful in the diagnosis, prevention
colypeptides. ADGUC sequences are useful in the diagnosis, prevention
and treatment of cardiovascular disorders (e.g. anglina pectoris,
myocardial infarction, ischemic heart disease, hypertension and
atherosclerosis), vision disorders (e.g. keratoconjuctivitis sicae,
keratitis, iritis, cataract), neurological disorders (e.g. epilepsy,
Alzheimer's disease, Pick's disease, Huntington's disease, dementia,
Parkinson's disease, Dick's disease, Huntington's disease, dementia,
Parkinson's disease, Creutzfeldt-Jakob disease, stroke, schizophrenia,
mental disorders including mood and anxiety and prion diseases including
kuru), reproductive disorders (e.g. infertility, endometriosis,
impotence, uterine fibroid and gynaecomastia), smooth muscle disorders
(e.g. arrhythmias, asthma and migraine) and bacterial infections
contransgenic animals to model human diseases. They are useful in
somatic or germline gene therapy, ADGUC polynucleotides are also useful
contransgenic animals to model human diseases. They are useful in
somatic or germline gene therapy, ADGUC polynucleotides are also useful
translocation, inversion, etc. among normal, carrier or affected
individuals, ADGUC polypeptides are useful in a number of drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human adenylyl and guanylyl cyclases and polynucleotides encoding
the cyclases, useful for treating, diagnosing or preventing
cardiovascular, neurological, vision, reproduction and smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                techniques and in vaccines. The present sequence is human ADGUC-2 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 112-113; 116pp; English.
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Lu Y;
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detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                    -----CGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCA 1189
                                                                                                                                                                                TGCTCACCTTCCAGAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCT 1369
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 2084 TGCGCTGCACCCAGAAGCGGAAAGAAGAAGGCCATGATCGCCAAGATGAACCGCCAGA 2143
                                                                                                                      AAGACAACGGGGGACCCAAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCCTGA
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                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 16985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
                          GGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCC-
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2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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genes from Drosophila and
interactions -
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11-JUL-2000;
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                                                                                 GCAGCCCCTCTGCGGCCTCTGGTGCCCTGTTCTTTGTATACATCGCATACACGCTCC 124
                                                                                                                                 TCCCCATCCGCATGCGGGCTGCCGTCCTCAGCGGCCTGGGGCCTCTCCACCTTGCATTTGA 184
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                                    ACGTGGTGCTGGGCATCCTGGCGGCAGTGCAGGTCGGGGGGGCGCTTTCGCAGCAGACCCGC
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             21;
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ed. No. 2.4e-203;
Mismatches 365;
  Pred.
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73.5%;
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 Local Similarity
            Matches 1069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526
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                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed DNA
                                                                                                                                                  CCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGC
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                                                                                                       4827;
                                                                                                     Query Match 24.6%; Score 445.8; DB 23; Length Best Local Similarity 57.7%; Pred. No. 1.2e-108; Matches 913; Conservative 0; Mismatches 607; Indels
                                                                              Sequence 4827 BP; 1115 A; 1377 C; 1340 G; 995 T; 0 other;
discloses genomic DNA sequences (ABL16176-ABL30511), exsequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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Database

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Sequence 176, App Sequence 173, App Sequence 173, App Sequence 23, Appl Sequence 20, Appl Sequence 20, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 1358, Ap Sequence 2292, Ap Sequence 6, Appli Sequence 14458, A Sequence 14458, A Sequence 14458, A Sequence 14458, A Sequence 5, Appli	АВКТ	10; Length 1812; 0; Indels 0; Gaps 0; GGGCGCTTTCGCAGCAGAC 60
US-10-051-643-176 US-00-880-505-176 US-00-880-505-173 US-09-980-442-23 US-09-989-442-23 US-09-989-442-20 US-09-989-442-20 US-09-989-442-20 US-09-989-442-20 US-09-989-442-20 US-09-989-442-20 US-09-980-422-6 US-09-980-422-6 US-09-980-15-11 US-09-980-15-11 US-09-980-15-11 US-09-960-15-12 US-09-954-531-848 US-10-033-246-6	ALIGNMENTS 240 T. FOR CONGESTIVE 2 /472,667 /008,097 /924,757 /048,933 /708,661 ersion 4.0	Score 1812; DB Pred. No. 0; 0; Mismatches GGGGGGAGTGGGTGG
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22222 22222222222222222222222222222222	A SEGULT 1 Sequence 3, Application US/09750240 Sequence 3, Application US/09750240 Sequence 3, Application US/09750240 SERNEAL INFORMATION: APPLICANT: Hammon, H. K. APPLICANT: Insel, P. A. APPLICANT: Gao, M. TITLE OF INVENTION: FAILURE TITLE OF INVENTION: FAILURE TITLE OF INVENTION: GENE THERAPY F TITLE OF INVENTION: GALLURE PRIOR FILLING DATE: 1999-12-27 PRIOR PELLING DATE: 1999-12-27 PRIOR PELLING DATE: 1999-10-16 PRIOR FILLING DATE: 1997-09-05 PRIOR FILLING DATE: 1997-09-05 PRIOR FILLING DATE: 1997-06-16 PRIOR PELLING DATE: 1997-09-05 PRIOR PEL	Ouery Match Best Local Similarity 100 Matches 1812; Conservative 1 GTTAACGTGGTCCTGGCCA 1 GTTAACGTGGTCTTGGCCA 1 GTTAACGTGGTGTTGTGTTTTTTTTTTTTTTTTTTTTTT
44444444444444444444444444444444444444	SULT 1 -09-750-240-3 Eadennce 3, Applica Fatent No. US200201 GENERAL INFORMATION APPLICANT: Hammon, APPLICANT: Hammon, APPLICANT: Ping, APPLICANT: Ping, APPLICANT: Ping, APPLICANT: Ping, APPLICANT: Ping, APPLICANT: Ping, APPLICANT: Dor, FILE REFERENCE: 220 CURRENT APPLICATION DATE: PRIOR FILING DATE: PRIOR APPLICATION DRIOR FILING DATE: PRIOR FILING DATE: PRIOR APPLICATION DATE: PRIOR TILING DATE: PRIOR APPLICATION DATE: PRIOR TILING DAT	Match local Si les 1812; l GTTAA l GTTAA
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Oy Dp	121	CTCCTCCCCATCCGCATGCGGGCTGCCGCTCACGGGCCTCTCCACCTTGCAT 180
Qy Db	181	TTGATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCC 240
Oy Db	241	AATGTGCTGCTGTTCCTCTGCACCAACGTCATTAGCATCTGCACCACTATCCAGCAGG 300
QY Dp	301	GTGTCTCAGGGGCCATTCAGGAGACCGGAGTTACATCCAGGCCCGGGTCCACTG 360
Oy Dp	361	CAGCATGAGAATCGGCAGCAGGAGCGGCTGCTGCTGGGTATTGCCCCAGCACGTTGCC 420
Qy Dp	421	atggagatgaagagacatcaacacaaaaaagagacatgticcacaagatctacata 480
QY Db	481	CAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCA 540
oy D	541	TCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGAC 600
ογ	601	AAGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGT 660
Oy Dp	661	GTGTCAGGGCTGCCGGAGGCCCGGGCCGATGCCCACTGCTGGTGGAGATGGGGGTA 720
Qy	721	GACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACGTGTGAATGTGAACATGCGC 780
Oy Dp	781	GTGGGCATCCACAGCGGGGGGGGGCGCGCGCCCTTGGCTTGGGAAATGGCAGTTC 840
Oy Dp	841	GATGTGTGCAATGATGTGACCCTGGCCAACCACGTGGAAGCAGGAGCCGGGCTGGC 900
Oy Db	901	CGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCA 960
. YO	961	GGCCGTGGTGGCAAGGGCAACGGTACCTCAAGGAGCAGCATTGAGACTTTCCTCATC 1020
Oy Db	1021	CTGGGCGCCAGCCAGAAACGGAAAGGGAAAGGCATGCTGGCCAAGCTGCAGGGGACT 1080
Oy Db	1081	CGGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGG 1140
οy	1141	ACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATCCAGCAAAGACAACGG 1200

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                                                      US-09-750-240-5

Sequence 5, Application US/09750240

Patent No. US20020103147A1

GENERAL INFORMATION:

APPLICANT: Hammon, H. K.

APPLICANT: Ping, P.

APPLICANT: Gao, M.

TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART

TITLE OF INVENTION NUMBER: US 09/472,667

PRIOR FILING DATE: 1999-12-27

PRIOR FILING DATE: 1999-01-16

PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: US 08/708,933

PRIOR PILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: US 08/708,661

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-09-05

NUMBER OF SEQ ID NOS: 13
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APPLICANT: Insel, P. A
APPLICANT: Ping, P. A
APPLICANT: Post, S. R. APPLICANT: Gao, M.
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                                            Length
                                            DB 10;
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                                          Score 1808.4;
Pred. No. 0;
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 Windows Version 4.0
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                                           Query Match 99.8%;
Best Local Similarity 99.9%;
Matches 1809; Conservative
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 for
FastSEQ
; SOFTWARE: FastSEQ; SEQ ID NO 5
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   CONGESTIVE
                                                                                                                                         Score 1763.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                        Query Match 97.3%;
Best Local Similarity 98.7%;
Matches 1789; Conservative
                                                                                                                     ; ORGANISM: Homo sapiens
US-09-750-240-10
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                                                                                       APPLICANT: TOMINSON, James E.
APPLICANT: TOMINSON, James E.
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: CLOUNING AND CHARACTERIZATION OF A HI
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5028-01-0S
CURRENT APPLICATION NUMBER: US/10/201,000
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: US/09/474,076
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/070,904
PRIOR FILING DATE: 1997-07-01
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Pred. No. 0;
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                                                               Sequence 1, Application US/10201000 Publication No. US20020187540A1 GENERAL INFORMATION:
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; LOCATION: (145)..(3648)
US-10-201-000-1
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SOFTWARE: PatentIn Ver.
          2436 TCCTGAGTACTTC
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APPLICANT: INCRANION:
APPLICANT: Insel, P. A.
APPLICANT: Post, S. R.
APPLICANT: Post, S. R.
APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: US 09/402,667
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR PELING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: US 09/008,933
PRIOR FILING DATE: 1997-09-05
PRIOR PALLING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,933
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,611
PRIOR APPLICATION NUMBER: US 08/708,061
PRIOR APPLICATION NUMBER: US 08/708,001
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Publication No. US20030008371A1
GENERAL INFORMATION:
APPLICANT: Tomininson, James
APPLICANT: Tomininson, James
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5027-01-US
CURRENT FILING DATE: 1209-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1998-12-29
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1997-07-01
                                                                                           2153
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                                                                                                                     CCAGAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTA
          1974 CCAGAGAGAGCTTTGAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGCTTA
                                    CGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCC
                                             ACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTAATCACCGT
                                                                                         ACACTCCACCCTGATGCTTGGGATCTATGCCAGCATCTTCCTGCTGCTGCTAATCACCGT
                                                                                                         GCTGATCTGTGCTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTC
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Pred. No. 1.4e-231;
); Mismatches 525; Indels
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Matches 1277; Conservative
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LOCATION: (139
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                                                 ---AGGACAAGAACGCCCAGGAGGAGCGCTGAGGATGAAGTGGATGAGGTTTTCTGG
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Patent No. US20020081659A1
GENERAL INFORMATION:
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ORGANISM: HOMO S
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                                                                                                                                    Length 2601;
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Pred. No. 3.2e-
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LOCATION: (2520)
CHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (2572)
OTHER INFORMATION: n equals a,t,g,
US-09-925-297-352
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Patent No. US20020164632A1
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Best Local Similarity 64.5%;
Matches 515; Conservative (
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Matches 329; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCATCCGCATGCGGGCTGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGAT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 AGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTACATCCAGGCCCGGCT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTGCCAATGTGCTGTTCCTCTGCACCAACGTCATTAGCATCTGCACACACTATCC
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                                                                                                                                                                                                                                                                                                                             0; Mismatches 435; Indels
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE;
FILE REFERENCE: 5800-47
CURRENT PELIGATION NUMBER: US/10/121,911
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/99/412,210
PRIOR FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 3518
                                                                                                                                                                                                                                                                                                  15.7%; Score 284; DB 9; 56.4%; Pred. No. 1.4e-66;
                                                                                                                                                                                                                                 adenylate cyclase
                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 21529 at
NAME/KEY: CDS
LOCATION: (247)...(3480)
                                                                                                                                                                                                                                                                                                                             Matches 617; Conservative
                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                  COCATION: (0)
COTHER INFORMA
NAME/KEY: CDE
LOCATION: (24)
US-10-121-911-2
                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                          FEATURE:
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804 GCACTGCGCGTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGAC 863
1368 ACTGTGGGAGTCATCGGGCTGCAGAAGTGGCAGTACGACGTTTGGTCACATGATGTCAC 1427
                                                                                                                                                                                                                                                                                                     1548 CTACCTTCGGGAGCTAGGGGAGCCTACCTATCTGGTCATCGATCCACGGGCAGAGGAGGA 1607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   703 TGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGT 762
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITCCACAAGAICTACATACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAG 522
GGCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCCATCTCGCT
                                                                                                                   864 CCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAAC
                                                                                                                                                                                                                                                                                                                                                                     ACTECAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTTTGCCCGGTTTGACAAGCTGCCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTG
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                                                                                          744 GGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGT
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Pred. No. 2.2e-48;
0; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (43)..(4101)
; OTHER INFORMATION: Adenylate cyclase coding region US-09-751-100b-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Medical Research Council
TITLE OF INVENTION: Human Adenylate Cyclase;
FILE REFERENCE: P27948A
CURRENT APPLICATION NUMBER: US/09/751,100B
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 104
SEQ ID NO I
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Sequence 1, Application US/10071223

Patent No. US20020137174A1

GENERAL INFORMATION:

APPLICANT: Storm, Daniel R.

APPLICANT: Hacker, Beth

APPLICANT: Tomlinson, James E.

APPLICANT: Tomlinson, James E.

APPLICANT: Tomlinson, James E.

APPLICANT: Tomlinson, James E.

APPLICANT: OR Therapeutics, Inc.

APPLICANT: OR THEAPLICANTON: CUCLASE

FILE REPERENCE: 44481-5029-02-US

CURRENT APPLICATION NUMBER: US/10/071,223

CURRENT APPLICATION NUMBER: 05/10/071,223

CURRENT APPLICATION NUMBER: 05/10/071,223

FRIOR PILING DATE: 1999-12-29

FRIOR FILING DATE: 1999-07-01

FRIOR FILING DATE: 1999-07-01

FRIOR FILING DATE: 1997-07-01

FRIOR FILING DATE: 1997-07-01

FRIOR FILING DATE: 1997-07-01

FRIOR PELING DATE: 1997-07-01

FROM APPLICATION NUMBER: 08/886,440

FROM APPLICATION NUMBER: 08/806,440

FROM APPLICATION NUMBER: 08/806,440
1606 CAGCTGGGAGTGGCAAAGTTCACATATCTGAGGCCACTGCAAAATACTTAGACGAC 1665
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                                                                                                                                                                                823 TTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAA 882
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                                                                           763 GTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGCACTGCGGCGTCCTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.6%; Score 209.4; DB 12; Length 4985; Best Local Similarity 62.1%; Pred. No. 2.3e-46; Matches 330; Conservative 0; Mismatches 201; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         1666 AGGTATGAAATGGAAGATGGGAGAGTTATTGAGCGC 1701
                                                                                                                                                                                                                                                                                                                                                                                           943 GACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGC 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: human type IX adenylyl cyclase FEATURE:
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LOCATION: (17)..(3898)
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US-10-071-223-1
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1945 GATCAAGGCCATCGAGGAGTTCTGCCAGGAGAAGAAGGAGATGGTGAACATGAGAGTCGG 2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1645 GAAGAAAAGTCTTCCATCCAAAAGCTCCTATAGCCTTCCGCCCTTTTAAGATGCAGCA 1704
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                                                                                                                                             AGGGCTGCCGGAGCCCGGGCCGACCATGCCCACTGCTGTGGAGATGGGGGGTAGACAT
                                                                                                                                                                                          GTGGTCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCAT
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                                                                                                                                                                                                                                                                       906 CCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGA 956
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Patent No. US20020142436A1
GENERAL INFORMATION:
APPLICANT: Wedical Research Council
TITLE OF INVERTION: Human Adenylate Cyclase and Use Therefor FILE REFERENCE: P27948A
CURRENT APPLICATION NUMBER: US/09/751,100B
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
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Pred. No. 6.5e-46;
0; Mismatches 202;
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62.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.0°
Matches 329; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (539)..(4600)
; OTHER INFORMATION:
US-09-751-100B-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  US-09-751-100B-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 98
LENGTH: 5515
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999
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CURRENT APPLICATION NUMBER: US/09/989,442
CURRENT APPLICATION NUMBER: US/119,065
PRIOR PRILING DATE: 2001-11-12
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-08-14
PRIOR PRILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/236, 369
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/234, 519
PRIOR FILING DATE: 2000-09-21
PRIOR PRILING DATE: 2000-09-21
PRIOR PRILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234, 519
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234, 519
PRIOR FILING DATE: 2000-09-21
PRIOR PRILING DATE: 2000-09-21
PRIOR
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FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/251,856
FILING DATE: 2000-12-08
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APPLICATION WUMBER: 60/251,868
FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/229,344
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FILING DATE: 2000-11-01
APPLICATION NUMBER: 60/225,268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-09-01
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2005 GGTGCACACGCGCACCGTCTTGCGGCATCCTGGGCATGAGGGTTAAATTTGACGT :2064
                                                                                                                                              2065 GTGGTCCAACGATGTGAACCTGGCCAATCTCATGGAGCAGCTGGGAGTGGCCGGCAAAGT 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ccKGGCCATCAGGAAACTGCGGGCAGCCACTGGCGTGGACATCAACATGCGTGTGGGCGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789 CCACAGGGGGGGGGGGACTGCGGCGTCCTTGCGGAAATGGCAGTTCGATGTGTG 848
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                                                                                     846 GTGGTCCAATGATGACCCTGGCCAACCACGAGGAGCAGGAAGCCGGGCTGGCCGCAT
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                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENDITON: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 182
LENGTH: 330
                                                                                                                                                                                                        906 CCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 71, Application US/09989442
Publication No. US20030013649A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 6.9%; Score 124.4; DB 9; Best Local Similarity 64.2%; Pred. No. 5.3e-24; Matches 185; Conservative 0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
CATTON: (289)
COTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (272)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: SITE
LOCATION: (285)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 182, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
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US-09-989-442-71
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PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/236,367
PRIOR APPLICATION NUMBER: 60/236,367
PRIOR APPLICATION NUMBER: 60/237,039
PRIOR PILING DATE: 2000-10-02
PRIOR PELICATION NUMBER: 60/237,038
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/236,370
PRIOR APPLICATION NUMBER: 60/236,802
PRIOR APPLICATION NUMBER: 60/236,802
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02 R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,513
R FILING DATE: 2000-09-05
R APPLICATION NUMBER: 60/231,413
R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/229,509 DR FILING DATE: 2000-10-13
DR APPLICATION NUMBER: 60/241,767
DR FILING DATE: 2000-10-20
DR APPLICATION NUMBER: 60/246,474
DR FILING DATE: 2000-11-08
DR APPLICATION NUMBER: 60/246,532
DR APPLICATION NUMBER: 60/249,216
DR FILING DATE: 2000-11-17
DR FILING DATE: 2000-11-17
DR FILING DATE: 2000-11-17
DR FILING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/249,210
DR FILING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/226,681
DR FILING DATE: 2000-11-17
DR FILING DATE: 2000-08-22 R FILING DATE: 2000-09-27

R APPLICATION NUMBER: 60/230,438

R FILING DATE: 2000-09-06

R RAPLICATION NUMBER: 60/215,135

R FILING DATE: 2000-06-30

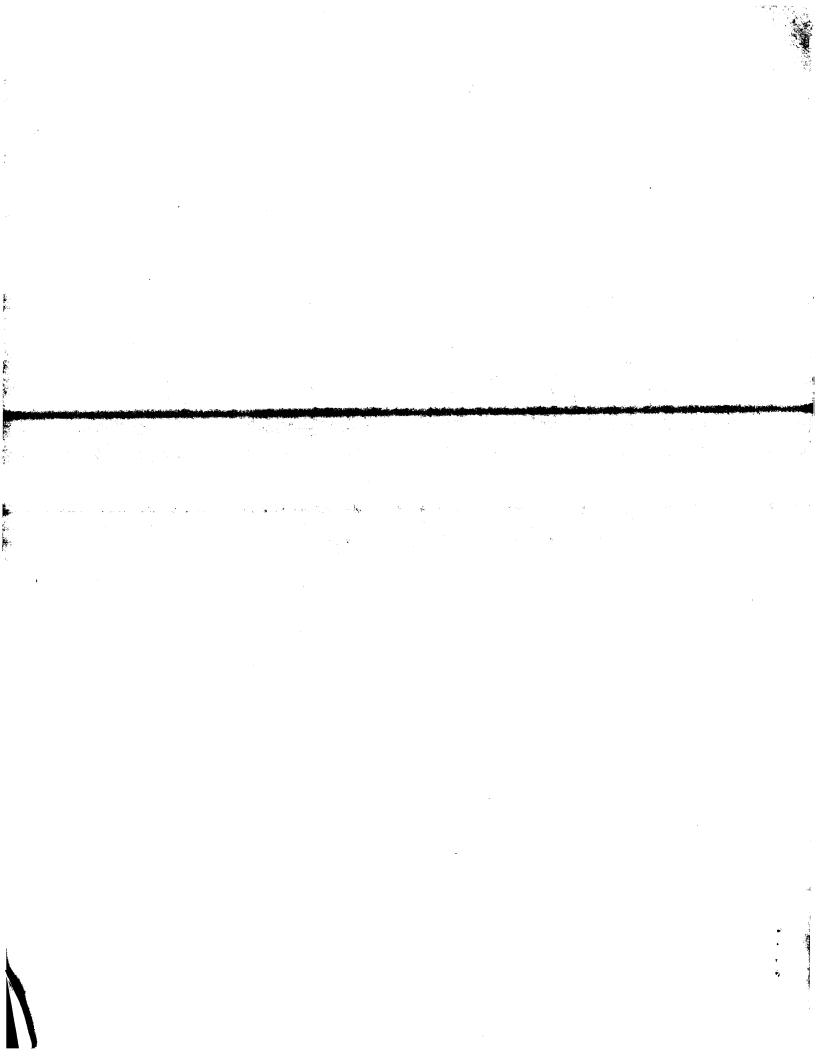
R APPLICATION NUMBER: 60/225,266 APPLICATION NUMBER: 60/229,287 FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/229,345 FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/239,935
FILING DATE: 2000-10-13
APPLICATION NUMBER: 60/239,937 FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/227,182
FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/225,214 FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/249,218
FILING DATE: 2000-11-17 FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,212 FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/225,213 APPLICATION NUMBER: 60/249,208 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,245 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/225,759 APPLICATION NUMBER: 60/235,836 APPLICATION NUMBER: 60/249,213 APPLICATION NUMBER: 60/249,207 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,244 FILING DATE: 2000-08-14 PRIOR PRIOR

729 TGAGGCCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCAT 788 61 CCKGGCCATCAGGAAACTGCGGGCACTGCCGTGGACATCAACATGCGTGTGGGGCGT 120 669 GCTGCCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGGAGATGGGGGTAGACATGAT 728 789 CCACAGCGGCGCGCGTGCACTGCGGCGTTGGCTTGCGGAAATGGCAGTTCGATGTGTG 848 Length 330; CATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGA 956 Indels 6.9%; Score 124.4; DB 9; 64.2%; Pred. No. 5.3e-24; tive 0; Mismatches 103; PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,217
PRIOR PAPLICATION NUMBER: 60/249,211
PRIOR PILING DATE: 2000-11-17
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR PELING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-09-11
PRIOR PELING DATE: 2000-09-11 Best Local Similarity 64.2 Matches 185; Conservative Similarity Query Match δ d d δ Q ōλ g g ò

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Fatent No. US20020061521A1
GENERAL INFORMATION:
TITLE OF INVENTYON: NOLE al.
TITLE OF INVENTYON: NUMBER: US/09/764,869
CURRENT PELLING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper; NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 445
LENGTH: 330
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Fatent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVERTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT FILING DATE: 2001-01-17
FILIS OF THE PROBLEM OF THE TOWNER OF SEQ ID NOS: 1510
SCHENAR OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
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COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (285)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
COTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-445
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-764-868-1351
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US-09-764-869-445
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                                                    Gaps
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                        4.4%; Score 79.2; DB 9; Length 11881; 63.4%; Pred. No. 5.2e-11; tive 0; Mismatches 78; Indels 1;
                                                                                                                                                                                                                                                         925 CIGCAGIACCIGAACGGGGACIACGAAGIGGAGCCA 960
                                                                                                                                                                                                                                                                                                              Search completed: March 1, 2003, 09:04:11
Job time : 106.396 secs
                                                     Conservative
                                    Best_Local Similarity
Matches 137; Conserv
US-09-764-868-1351
                            Query Match
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APPLICANT: Hammond, H. Kirk
APPLICANT: Hammond, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Ping, Perbel
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
ADDRESSES: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
       US-08-997-080-176
US-08-997-362-176
US-09-324-542-176
US-09-324-542-176
US-09-205-426-173
US-08-997-362-173
US-08-997-362-173
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US-09-135-011-79
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APPLICATION NUMBER: US/09/008,097
FILING DATE:
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REFERENCE/DOCKET NUMBER: 22000-20567.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-413-5600
TELEPA: 650-494-0792
TELEX: 70614
                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                    Sequence 3, Application US/09008097 Patent No. 6306830 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER M
REGISTRATION NUMBER: 37,61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Coding Sequence LOCATION: 1...1812 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H: 1812 base pairs
nucleic acid
DEDNESS: double
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CITA.
STATE: CA
COUNTRY: USA
TO: 94304-1018
 STRANDEDNESS:
 RESULT 1
US-09-008-097-3
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 604
8001284888888444444
800128459286012845
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Sequence 1, Appli
Sequence 11, Appli
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Sequence 15, Appli
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Sequence 13, Appli
Sequence 3, Appli
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12520.796 Million cell updates/sec
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                                                                       February 28, 2003, 22:03:11; Search time 44.382 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5,
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Sequence
Sequence
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Sequence J
Sequence J
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1812
1 9ttaacgtggtgctgggcat......gcagctttcctgaggtgttc
                                                                                                                                                                                                                                                                                                                       1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-997-362-123
US-09-095-855-123
US-09-324-542-123
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US-09-008-097-5
Sequence 5, Application US/09008097
Patent No. 6306830
GENERAL INFORMATION:
APPLICANT: Hammond, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Ping, Peipei
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOI
TITLE OF INVENTION: HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                       OPERATING SYSTEM: DOS , SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1808.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                         37,612
SR: 22000-20567.21
                                                                                                                                                 US/09/008,097
                                                                                                                                                                                                                                          NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 220C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
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 ROAD
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99.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 1...3501 OTHER INFORMATION:
                                           COMPUTE: 519: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 3549 base pairs
                                                                                                                                  CURRENT APPLICATION DATA:
755 PAGE MILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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              PALO ALTO
                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                       706141
                                        USA
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                                        COUNTRY:
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                                               Length 4942;
                                                                                                                                                                                                                                                                                          APPLICANT: TOOR Therapeutics, Inc.
APPLICANT: TOOR Therapeutics, Inc.
TITLE OF INVENTION: CLOUNG AND CHARACTERIZATION OF A HUM;
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5028-01-US
CURRENT PAPLICATION NUMBER: US/09/474,076
CURRENT FILING DATE: 1999-12-12
PRIOR FILING DATE: 1999-12-07
PRIOR PRIOR PELICATION NUMBER: 60/070,904
PRIOR PELICATION NUMBER: 60/070,904
PRIOR PELICATION NUMBER: 08/886,550
PRIOR PELICATION NUMBER: 08/886,550
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VOY: 2.0
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                                                                                                                                                                                                                                                            Sequence 1, Application US/09474076
Patent No. 6465237
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: human type VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1
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Matches 1788; Conserv
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09-474-076-1
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                                        365 ATGAGAATCGGCAGCAGGAGCGGCTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGG
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                                            2402 TGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGGAGCTGTG
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                                                                                                                      GCAGCATTGTCCGCTCACGGCCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yoshihiro Ishikawa
TITLE OF INVENTION: Cloning and Character-
TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Alan M. Gordon
ADDRESSEE: American Cyanamid Company
STREET: 1937 West Main Street,
STREET: P.O. Box 60
CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/07/793,961A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203 321 2719
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SOFTWARE: ASCII from DW4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy Disk
IBM PC AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLING DATE: 19911118
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
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FILING DATE: 19911118
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STATE: Connecti
COUNTRY: USA
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                                                                                                     Length 4046;
                                                                                                     Score 1519.8; DB 1; Length
Pred. No. 0;
0; Mismatches 162; Indels
                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                       83.9%;
90.7%;
                                                                                                                        Best_Local Similarity 90./
Matches 1643; Conservative
                 single
               STRANDEDNESS
; TYPE: NUC;
; STRANDEDNE;
; TOPOLOGY:
; MOLECULE TYP!
US-07-793-961A-1
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                               TGGCCCCAGCCAGAAACGGAAAGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTC
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Patent No. 5578481
GENERAL INFORTION:
APPLICANT: ISBIRAWA, YOSHINITO
TITLE OF INVENTION: Cloning and Characterization
TITLE OF INVENTION: Cardiac Adenylyl Cyclase
UNMARER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,357
FILING DATE: 10-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                             NAME: Gordon, Alan M.
REGISTATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31,70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-324
TELEPHONE: 201-831-326
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.9%;
Best Local Similarity 90.7%;
Matches 1643; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4046 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
One Cyanamid
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                                 New Jersey
                                                                  07470-8426
                                             USA
                Wayne
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; LOCATION:
US-08-240-357-1
              CITY: Way
STATE: Ne
COUNTRY:
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2499 ATTACTCTCTGGGCCTGGATGCTCCGCTGTGAGGGCACCGCACCCACTTGCAGCTTCC 2558
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                                                           5 ACGTGGTGCTGGGCATCCTGGCGGCAGTGCAGGTCGGGGGGGCGCTTTCGCAGCAGACCCGC
ATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTC
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APPLICANT: Tang, Wel-Jen
APPLICANT: Tang, Wel-Jen
APPLICANT: Gliman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: CONCULTENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.3%; Score 1437.2;
87.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
RESISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
                                                                                                                                                                                                                                                                                                                                                                            America
                                                                                                                                                                                                                Sequence 11, Application US/08726214 Patent No. 6107076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4131 base pairs
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COUNTRY: Uni
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US-08-726-214-11
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            TGTCAGGGCTGCCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAG 721
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                                               AGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTG
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Sequence 1, Application US/09473716

Patent No. 6436672

GENERAL INFORMATION:

APPLICANT: Tomlinson, James

APPLICANT: Tomlinson, James

TITLE OF INVENTION: CLCLASE

TITLE OF INVENTION: CYCLASE

TITLE OF INVENTION: CYCLASE

FILE REPERENCE: 44481-5027-01-0S

CURRENT FILING DATE: 1999-12-29

PRIOR PPLICATION NUMBER: PCT/US98/13540

PRIOR PLILING DATE: 1998-07-01

PRIOR PLILOR INVENTION NUMBER: 60/070, 901

PRIOR PLILOR APPLICATION NUMBER: 08/086, 362

PRIOR PLILOR DATE: 1997-07-01

PRIOR PLILOR DATE: 1997-07-01

SOFTWARE: PALENTING DATE: 1997-07-01
   1887 GTGCCCAAGATGCTCTGAACCCTGAGGATGAGGTGGACGAGTTTCTGGGGCCGAGCCATCG 1946
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                                                                                   TTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCTAATTTTCCCAC
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; LOCATION: (139)..(3921)
US-09-473-716-1
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1490 TAATCACTGTGTGTGTGTGTGTGTGTACTCCTGCGTAAAGCTCTTCCCCTCCCCACTGC

2540 CCTTGGTGGTGTTTTGTGTCTGTGATCTACTCCTGCGTAAAGCTCTTCCCCTCCCCCACTGC
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APPLICANT: Tang, wei-Jen
APPLICANT: Tang, wei-Jen
APPLICANT: Tang, alired G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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; Sequence 9, Application US/08726214
; Patent No. 6107076
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                                                                                                                                                                                                                                                                 Score 858.2; DB 3;
Pred. No. 1.5e-219;
0; Mismatches 548;
                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: 0750:450
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                   47.48;
68.68;
Floppy disk
                                                                                                                                                                                                     LENGTH: 3924 base pairs
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Matches 1254; Conservative
                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                             -08-726-214-9
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TGTCAGGGCTGCCGGAGCCCGGGCCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAG
                     ------CGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGCTTCCAGCA
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                                                                                              GAGATGGGGGTAGACATGATTGAGGCCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAAAT
 289 TATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTACATCCAGGCC
                                                                         349 CGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGGCTGCTGCTGTCGGTATTGCCC
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                                      805 ATCCTGGCTGAGCGCGCCCAGAGGAAGGCCTTCCTGCAGGCCCGGAACTGCATTGAGGAC
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Patent No. 6107076

GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLXL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CITY: Houston
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ADDRESSEE: Arnold, W
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1730 TGCAGCAG-----CTCAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCA 1783
                     172 ACCTIGCATTIGATCTIGGCCTGGCAACTTAACCGTGGTGA----TGCCTTCCTCTGGAAG 228
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                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: CONCULTENTLY Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 436; DB 3;
Pred. No. 1e-106;
                                                                       1784 TGCCCACCTGCAGCTTTCCTGAGGTGTTC 1812
                                                                                              2215 AGTCCAACTGCAACTTCCCAGAGTACTTC 2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                         Sequence 1, Application US/08726214
Patent No. 6107076
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66.0%;
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3978 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 66.0
Matches 647; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                    RESULT 9
US-08-726-214-1
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1090 ATGTCCTACTACATGGCAGACCGTAAGCACCGAAAGGCCTTCCTGGAGGCCCGCCAGTCG 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 CTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGCTCTCTGCACCAACGTCATTAGCATC
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                                                                                                                                                                                                                                                                                      MAMMALIAN ADENYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
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Pred. No. 7.6
                                                                                                                                                              US-08-726-214-5

Sequence 5, Application US/08726214

Patent No. 6107076

GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN AD
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      RY: United States of America 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: UTSD:450 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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63.6%;
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EDNESS: single
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                                                       1015 CTCATCCTGGGCGC
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Best Local Similarity
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             PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 393.2; DB 3
Pred. No. 1.9e-95;
                                                                                CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/005,498

FILING DATE: 04-0CT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REERENCE/DOCKET NUMBER: UTSD:450

TELECOMMUNICATION INFORMATION:

TELEFAN: (512) 418-3000

TELEFAN: (512) 474-757

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
                                                 APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.7%;
71.0%;
                                                                                                                                                                                                                                                                                                                                     1652 base pairs
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Best Local Similarity 71.0°
Matches 521; Conservative
                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                     GACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTA 747
                                                                                                                                                                                                                                    CGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGGGGGGCGCGTGCAC 807
                                                                                                                                                                                                                                                                                                   AGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGGGGCC
                                                                                                                                                                                                                                                                                                                                    GCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGGCAACACTG
                                    TTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                     CAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SOUTHNESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FLILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6107076
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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US-08-726-214-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 CGGGCTGCCGTCCTCAGCGGCCTGGGCCTCCACCTTGCATTTGATCTTGGCCTGGCAA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCAACACAAAAAAAAAGAAG-----ACATGTTCCACAAGATCTACATACAGAAG 486
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                                                                                                                                                                                                                                                                                                                                                                                           79 GGCCTCTGGTGCCCTGTGTTTTGTATACATCGCATACACGCTCCTCCCCATCCGCATG 138
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                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                    Score 320.6; DB 3; Length
Pred. No. 7.8e-76;
0; Mismatches 374; Indels
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                     TELEPHONE: (512) 418-3000
TELEFAX: (512) 447-757
INFORMATION FOR SEC ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    17.7%;
59.5%;
                                                                                                                         LENGTH: 4601 base pairs
                                                                                                                                                                                                                                                                                                               Best_Local Similarity 59.5
Matches 567; Conservative
                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                           linear
                                                                                                                                                                                                           ; TOPOLOGY:
US-08-726-214-15
                                                                                                                                                                                                                                                                                       Query Match
Best Local
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1450 GGTGGTGACCGACACTACATGCCCGACAACAACTTTCACAGCCCTCTATGTCAAGCGGCAC 1509
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60.7%;
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Best Local Similarity 60.7'
Matches 503; Conservative
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                              GGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACTTGAGACTTTCCTCAT 1019
                                                Length 5199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tang, Wel-Jen
APPLICANT: Tang, Wel-Jen
APPLICANT: Gliman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: CONCURRENTLY Herewith
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Pred. No. 2.7e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Highlander, Stewen L.
REGIESTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 5199 base pairs
TYPE: nucleic acid
STRANDENNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                               Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                                                                      Sequence 13, Application US/08726214 Patent No. 6107076
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Best Local Similarity 62.2%;
Matches 524; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, Wh:
STREET: P.O. Box 4433
CITY: Houston
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                                                                                                                                                                                                                                                                                                                               Texas
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                                                                                                                                                                                                                                                                                                                          STATE: Texas
COUNTRY: Un
ZIP: 77210
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US-08-726-214-13
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1929 GGCAAGCGCAACGCGTACCTCAAGGAGCAGCACTTTGAGACTTTCCTCATCCTGGGCGCC 1029 2049 CTGCCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGGAGATGGGGGGTAGACATGATT 729 909 219 CCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAACGTCATTAGCAT 278 279 CTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTA 338 Gaps GCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGG GAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATC CACAGCGGGCGCGTGCTGCGCGTCCTTGCCGCAAATGGCAGTTCGATGTGTGG TCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCAC 910 ATCACTCGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGT ACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCT 30; Length 4008; GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: OYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
FILE REFERENCE: 29770
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0 Indels Score 286; DB 3; I Pred. No. 1.3e-66; 0; Mismatches 295;

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1284 GICICAIGAIGITACICIGGCAAACCACAIGGAAGCIGGAGGAGICCCIGGGCGIGIICA 1343
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                                                                                                               CATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGCAGCGGCTGCTGCTGTC
                                                                                                                             489 TGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTG
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                                                      399 GGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 31
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ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
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US-08-726-214-3
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279 CIGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTA 338
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                                                                                                                                                                                                                                                                                                                                           15.8%; Score 286; DB 3; 60.7%; Pred. No. 1.3e-66;
UMBER: US/08/726,214
Concurrently Herewith
             FILING DATE: Concurrently Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 UTSD: 450
                                                                                                           NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REPERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEFAX: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUINCE CHARACTERISTICS:
LENGTH: 4008 base pairs
TYPE: nucleic acid
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Search completed: March 1, 2003, 04:05:16 Job time : 85.382 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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February 28, 2003, 21:13:01; Search time 3111.21 Seconds (without alignments) 16949.756 Million cell updates/sec 1 gttaacgtggtgctgggcat.....gcagctttcctgaggtgttc 1812 4109280 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 US-09-750-240-3 1812 Title: Perfect score: Scoring table: Database : Searched: Sequence: Run on:

GenEmbl:*

1: 9b.ba:*
2: 9b.htg:*
3: 9b_htg:*
4: 9b_on:*
5: 9b_on:*
6: 9b_pt:*
6: 9b_pt:*
10: 9b_pt:*
11: 9b_st:*
11: 9b_st:*
12: 9b_st:*
13: 9b_pt:*
13: 9b_pt:*
14: 9b_st:*
13: 9b_n:*
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15: em_ba:*
16: em_fun:*
17: em_hun:*
18: em_pa:*
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22: em_ov:*
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33: em_htg_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	· · · · · ·	741 0000 V V 1844 W 000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			ID AR174472 AR189759 AR189761 AX189766 AX189766 AX189766 AX189766 AX189766 AX189766 AX106658 AX305965 AX305965 AX305967 AX305965 AX305965 AX305965 AX305967 AX30597 AX30597 AX30597 AX30597 AX30597 AX30597 AX30597 AX30597 AX30597		Description AR174472 Sequence AX189759 Sequence AX189765 Sequence AX189766 Sequence AX189766 Sequence AX189766 Sequence AX189768 Sequence AX189768 Sequence AX189768 Sequence AX189768 Sequence AX189768 Sequence M96653 Mus musculu AX305965 Sequence M96100 Rattus norv AX305965 Sequence M9410115 Rattus norv AX305965 Sequence M9410115 Rattus norv AX406596 Sequence M941015 Rattus norv AX406596 Sequence M9410658 Sequence M9410659 Rattus norv	nnce nnce nnce nnce sapi sapi sapi sapi e 1 nore nnce adeny nnce adeny nnce adeny nnce adeny nnce nnce nnce nnce 1 nnce 1
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RESULT 1 AR174472 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES		2262	from pe GI:17' GI:17' ad. i to 18' i'ir', i'y for' 630683'	n patent:1791479:1812) ', Insel 683 conge:683 conge:	ALIGNMENTS 1812 bp t US 6306830. 92 1,P.A., Ping,Pestive heart f 3 23 oCT-2001; 11fiers	1 t, S	ear PAT 17	-DEC-2001

Qy 961 GGCCGTGGTGGC7 	1021	1081	1141	1201	1261	1321	0y 1381 GTTGCCTGTGCCC Db 1381 GTTGCCTGTGCCC	1441	0y 1501 CTCATCTGTGCTC	1561		1681	1741	Oy 1801 CCTGAGGTGTTC 	AX189759	NOI	SOURCE numan. ORGANISM HOMO sapien Eukaryota; Mammalia; E REFERENCE 1 (bases 1
	DB 6; Length 1812; 0; Indels 0; Gaps 0;	CGGGGGCGCTTTCGCAGCAGAC 60	CTTTGTATACATCGCATACACG 120	CCTGGGCCTCTCCACCTTGCAT 180	CCTCTGGAAGCAGCTGGTGCC 240	CTGCACACACTATCCAGCAGAG 300	CATCCAGGCCCGGCTCCACCTG 360		CATGITCCACAAGAICIACATA 480	TGAGGGCTTCACCAGCCTGGCA 540	.rgagcrcrtrgcccggrrrgac 600	CTTGGGGACTGTTACTGT 660	CTGCTGTGTGGAGATGGGGTA 720	AGGTGTGAATGTGAACATGCGC 780	TGGCTTGCGGAAATGCAGTTC 840	GGAAGCAGGAAGCCGGGCTGGC 900	CGGGGACTACGAAGTGGAGCCA 960
source 11812 /organism="unknown" Aorganism="unknown" 707 g 405 to 108	Query Match 100.0%; Score 1812; Best Local Similarity 100.0%; Pred. No. 0; Matches 1812; Conservative 0; Mismatches	1 GTTAACGTGGTGCTGGGCATCCTGGCGGCGGTGCAGGTCGGGGCGCTTTCGCAGCAGAC	61 CCGCGCAGCCCTCTGCGGGCCTCTGGTGTTCTTTGTATACATCGCATACACG	121 CTCCTCCCCATCCGCATGCGGGCTGCCGTCGCGGGCCTGGGGCCTCTCCACCTTGCAT	181 TIGATCTIGGCCTGGCAACTIAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGGTGCC	241 AATGTGCTGTTCCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAG	301 GTGTCTCAGCGCCAGGCCTTTCAGGAGCCCGCAGTTACATCCAGGCCCGGCTCCACTG	361 CAGCATGAGAATCGGCAGCAGGAGCGGCTGCTGTGTCGGTATTGCCCCAGCACGTTGCC	421 ATGGAGATGAAAGACATCAACACAAAAAAAGAAGACATGTTCCACAAGATCTACATA 	481 CAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCA 11111111111111111111111111111111111	541 TCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGAC	601 AAGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGT	661 GTGTCAGGGCTGCCGGAGCCCGGGCCGATGCCCACTGCTGTGTGGAGATGGGGGTA	721 GACATGATĤGAGGCCATCTCGCTGGTGAGGTGACAGGTGTGAGATGTGAACATGCGC 	781 GTGGGCATCCACAGCGGGCGCGTGCACTGCGGCTCCTTGGCTTGCGGAAATGGCAGTTC	841 GATCTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGC	901 CGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCA
BA OR.		QQ Op	qa o	Q D	Oy Dp	Q Dp	oy Dp	Oy Dp	oy Dp	QY Dp	QY Db	OY Db	Q Dp	Q B	Oy Dp	Oy Dp	à g

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linear PAT 08-AUG-2001
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: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            CAGAAACGGAAAGAGAAAAGGCATGCTGGCCAAGCTGCAGCGGACT
                                                           ATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTC
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3 from Patent WO0148164.
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AUTHORS		qu	841 G
JOURNAL	Patent: WO 0148164-A 3 05-JUL-2001;	QY	901
FEATURES	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) Location/Qualifiers	qa	901
inos	ce 11012 /organism="Homo sapiens"	δ	961
BASE COUNT	361 a	qα	961
Ouera	100 08. CANA 1013. NO 6. IANA 101	Qy	1021
Best Loc	sacm 100.0%; Scote 1012; UB 0; Length 2018 Similarity 100.0%; Pred. No. 0; Dr. 1913: Conservative 0: Mismatches 0: Indels	qq	1021
- T	03 CKCKCCKECKEEECCCCCCCCCCCCCCCCCCCCCCCCC	QY	1081
		QQ	1081
9		Oy	1141
	12	qa	1141
Qy 121		QY	1201
_ Db 121		qq	1201
Qy 181	TTGATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCC 240	QY	1261
Db 181		qα	1261
0y 241	AATGTGCTGCTGCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAG 300	Oy	1321
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	GTGTCTCAGCGCCCAGCCCTTCAGGAGCCCGCAGTTACATCCAGGCCCGGCTCCACCTG 360	&	1381
	36	δŏ	1441
Qy 361	CAGCATGAGATCGGCAGCAGCAGCAGCTGTTGTTTTGCCCCAGCAGTTGCC 420	qq	1441
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0v 481	יי	QY	1561
		QQ	1561
		QY	1621
		qa	1621
Qy 601		ογ	1681
Db 601		qa —	1681
Ωγ 661	GTGTCAGGGCTGCCGGAGCCCGACCATGCCCACTGCTGTGGAGATGGGGGTA 720	0y	1741
_ Db 661		qq	1741
Qy 721	GACATGATTGAGGCCATCTCCCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGC 780	δδ	1801
Db 721	GACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGTGAGGTGTGAATGTGAACATGCGC 780	q	1801
Oy 781	GTGGGCATCCACAGCGGCGCGTGCACTGCGGCGTCCTTGGCTTGCGGAAATGGCACTTC 840	RESU AR17	RESULT 3 AR174473
	GATGTGTGCTCCAATGATGTGACCCTGGCCAACATGGAAGAGAGAAGAGAGATGGCGGCTGGC 900	DEFIN	DEFINITION ACCESSION
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PAT 17-DEC-2001
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ATGTGTGTCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGC
                                                                                             TGGGCGCCAGCAGAAACGGAAAGAGAGAAAAGGCATGCTGGCCAAGCTGCAGCGGACT
                                                       GCCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATC
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Sequence 5 from patent US 6306830.
AR174473 GI:17914793
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GATCTGTGCTGTGTACTCCTGTGGTTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCG
                                                                                                            CAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAAACGGGG
                                                                                                                                                                          CACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGA
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Hammond, H. K. and Gao, M.
Gene therapy for congestive heart failure
Patent: WO 0148164-A 10 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                             AX189766.1 GI:15143139
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2436 TGAGGTGTCC 2445
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SCLRDAEPPSPTPAGPPRCPMQDDAFIRRGGPGKGKELGLRAVALGFEDTEVTTTAGG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1740 CAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTT 1799
                            2376 CAATTACTCTCTGGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGGTT 2435
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Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
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/organism="Homo sapiens"
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Hammond, H. R. and Gao, M.
Gene therapy for congestive heart failure

ORGANISM

REFERENCE AUTHORS TITLE

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                                                                                                                                                9
                                                                                                                          Length
                  (ns)
9
                                                                                                                                                77;
                                                                                                                           DB
                                                                                                                       Score 1657.8;
Pred. No. 0;
0; Mismatches
                                                                                                                          Query Match 91.5%;
Best Local Similarity 95.4%;
Matches 1730; Conservative
                                            source
                                                                                        BASE COUNT
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Euteleostomi; Homo.

SK

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Direct Submission
Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarauu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:2887418.

Location/Qualifiers
1. 5877
/organism="Homo sapiens"
//dx.ref="taxon:966"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BaA24852.2"
| Decein_id="BaA24852.2"
| Aranslation="ESTRAGGTARTRGLGGPRDGRPAGRSPRGRGGGPGQARSRAGS
| MMSWFSGLLVPRVUDERKTAMGERNGQKRSRRRGTRAGGFCTPRYMSCLRDAEPPSPTP
                                                                             Ishikawa, K., Nagase, T., Nakajima, D., Seki, N., Ohira, M., Ohyatima, H., Ingaka, A., Kotani, H., Nomura, N. and Ohara, Order Prediction of the coding-samences of unidentified human genes.

VIII. 78 new cDNA clones from Dean which code for large proteins
                                                                                                                                                                                                                                                                                                                                                                /sex="male"
//tissue_type="bracin"
//clone_lib=_pBluescriptII SK plus"
//note="This sequence was obtained by subcloning of the fragments derived from two cDNA clones (1 - 1352 was derived from pg00161 and 1353 - 5877 was derived from h01205).
sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII clone:hh01205s1.
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                            4 (5), 307-313 (1997)
                                                                                                                                                                                                                                                                                                                                                    /clone="hh01205s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .5877
/gene="KIAA0422"
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ilarity 98.7%;
Conservative
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                 plus clone:hh
Homo sapiens
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AGPPRCPWQDPGSKGELGIRAVALGEEDTEVTTFAGGTAEVPDAPPER
AGPPRCPWQDPGSKGELGIRAVALGEEDTEVTTFAGGTAEVPDAPPER
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VTGVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHMEAGGRAGRIHITRATL
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LMFGNYTSTRIGNATAGOHETLIGASQKREEREMALAKLOOFTRANSMEG
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ARSIANSTYDQVGRRHITALADAYAMRLMEQNKHINBHSFNNROMKIGLNMGPVVAGV
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Pred. No. 0;
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us-09-750-240-3.rge

CCTCTGCGGGCCTCTGGTGCCCTGT
тстесте
ATGCGGCTGCCGTCCTC
GGCAACTTAACCGTGGTGAT(
CTCTGCACCAACGTCATT
CCAGGCCTTTCAGGAGACCCGCAG1
SCAGCAGGAGCGGCTGCTGC
saaagaagacatcaacacaaaaaaagagac-
CAATGTCAGCATCCTGTTTGCAGACATTG
TGCGCAGGAGCTGGTCATG
GGAGAATCACTGCCTGAGGAT
CCGGAGGCCGGGCCCACTG
GAGGCCATCTCGCTGGTACGTGAGGT(
CAGCGGCGCGTGCACTGC
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CACTCGGGCAACACTGCAGTAC
CAAGCGCAACGCGTACCTCAAGGAGC
SCCAGAAACGGAAAGGGGGGGAAAGG
CCATGGAAGGCTGATGCCGCGATGCC

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1 (bases 1 to 4046)

Katsushika, S., Chen, L., Kawabe, J., Nilakantan, R., Halnon, N.J., Honcy, C.J. and Ishikawa, Y.

Cloning and characterization of a sixth adenylyl cyclase isoform: types V and VI constitute a subgroup within the mammalian adenylyl cyclase family

Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)
1528892
                 1914 CCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCGGG 1973
                                                                                              2033
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1142 CCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCGGG 1201
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                                                                                1974 GCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGAGTTGAGTTCCTGAGCCGTGCCATCG
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1206 c 1254 g 843 t
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1. 4046
/organism="Canis familiaris"
/db_xref="taxon:9615"
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Best Local Similarity
Matches 1648; Conserv
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Oy 65 GCAGCCCTCTGGGGCCTCTGGTGCTTTTTTTTTTTTTTT	1002 1011111111111111111111111111111		1362 AGCTGGCTGCGGAAAATCACTCCTGAGGATCATTTTTTTT	OY 782 IGGGCATCCAAGGGGGGGGTATGGGGGGTTGGGGAATGGCGAATGGGGATTGG 841 Db 1542 IGGGCATCCAAGGGGGGGTGTGCTGGGTAATGGCGAATGGCAATTGG 1601 OY 842 ATGTGTGGTCCAATGATGTGCCTGGCCACTGGGGAATGGCCTGTCG 1601 OY 842 ATGTGTGGTCCAATGATGTGCCTGGCCACTGGGAAGCAGGAATGGCTGCC 901	QY 1022 TGGGCGCCAGCCAGAAACGGAAAGGGAAAGGCATGCTGGCCAAGCTGCAGCAGCTC 1081 III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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Premont, R.T.
Premont, R.T.
adultiple mechanisms underlying desensitization of the liver adenylyl cyclases system. Structure and cAMP regulation of liver adenylyl cyclases
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Premont, R.T., Jacobowitz, O. and Iyengar, R.
Lowered responsiveness of the catalyst of adenylyl cyclase to stimulation by GS in heterologous desensitization: a role for adenosine 3',5'-monophosphate-dependent phosphorylation
                                                                                                 1142 CCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCGGG
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/db_xref="taxon:10090"
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Pred. No. 3.2e-311;
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Tang.W.-J. and Gilman, A.G.
Soluble mammalian adenylyl cyclase an
Patent: US 6107076-A 11 22-AUG-2000;
Location/Qualifiers
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6107076.
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Matches 1584; Conservative
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/product="adenylyl cyclase type VI"
/protein_id="AAA40678.1"
/db_xref="G1:202719"
/translation="MPLPVARSGSGRSSMSWFSGLLVPRVDERKTAWGERNGGKRPRO
ATRARGFCAPRYMSCLKNVEPPSPTPAARTRCPWQDEAFIRRAGPGRGVELGLRSVAL
GFDDTEVTTPMGTAEVAPDTSPRSGPSCWHRLAQVFQSKQFPSAKLERLYQRYFFQMN
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Premont, R.T., Chen, J., Ma, H.W., Ponnapalli, M. and Iyengar, R.
Two members of a widely expressed subfamily of hormone-stimulated
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M96160
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adenylate cyclase; adenylyl cyclase type VI.
Rattus norvegicus (strain Sprague-Dawley) adult liver, kidney
heart cDNA to mRNA.
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Sciurognathi; Muridae; Murinae;
TCATCTGTGCTGTGCTCCTGTGGGTCTTTCTTCCCCCAACGCCCTGCAGCGCCTGTCCC
                                                                                         GCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCCATCTTTCCGTCCTGCTTG
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/db_xref="taxon:10116"
/tissue_type="liver, kidney, he
/dev_stage="adult"
/dc_number="4.6.1.1"
/citation=[2]
/citation=[1]
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A.
93028552
1409703
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Mammalia; Eutheria; Rodentia;
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Premont, R.T.
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SMWYOSYVUCILAANOPGRALAANPRSPSAGLWCPVEFYTITYILLDIRMRAANLG
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GAQDALNPEDEVDEFIGRAIDARSIDQLRKDHVRRFLLTFQREDLEKKYSRKVDPRFG
AYVACALLVPCFICFTOFTVPPRAAILGITYAGIFLLLTVTVULGAVSSGGSFPNAL
ORLSRSIVRSKYHSTANGVESVLLVFISAINAMFTCSHTPGLLGXVSGGFPPNAL
CHROLNYSIGLEAPLCGFTAPTCSFPEYVGSVLLSLLASSVFLHISSIGKLVMTFV
LGFTYLLLLLGSPATICFTANTALGATGSKEEMEELOAYNRRLLHINIPROVAHF
LVFALALY YGSCECYAWEASIANFSEFYDELBANNEGYECHLINEITARPDEI
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SFNNFOMKIGLNMGPVVAGVIGARROYVINGNTVNVSSRMDSTGVPDRIQVTTDLYQ
VLAAKGYQLECRGVVKVKGCEMTTYFLNGGPSS"
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79.3%; Score 1437.2; DB 10; Length 4131;
Best Local Similarity 87.5%; Pred. No. 3.2e-311;
Matches 1584; Conservative 0; Mismatches 223; Indels 3;
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oy P	722	ACATGATGAGGCCATCTCGCTGGTACGTCAGGTGACAGGTGTGAACATGCGCG 781 	
Oy Db	82	ATCCACAGCGGGCGGTGCACTGCGCGCGTTGGCTTGCGAAATGCAGTTCG 841	
oy Dp	842	ATGTGTGGTCCAATGATGTGACCCTGGCCAACCATGGAAGCAGGAAGCCGGGCTGGCC 901	
Qy Dp	902	GCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAG 961	
Qy Db	962	GCCGTGGTGCCAAGGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCC 1021	
oy Dp	1022	TGGGCGCCAGCCAGAAACGGAAAGGGAAAGGCATGCTGGCCAAGCTGCAGCGGACTC 1081	
Oy Dp	1082 1767	GGGCCAACTCCATGGAAGGCTGATGCCGCAGGGTTCCTGATCGTGCCTTCTCCCGGA 1141	
Oy Dp	1142	CCAAGGACTCCAAGGCCTTCCGCCAGATGGCATTGATGATTCCAGCAAAGACAACGGG 1201 	
ç a a	1202	GCACCCAAGATGCCTGAACCCTGAGGATGAGTGGATGAGTTCCTGAGCGGTGCCATCG 1261	
oy Dp	1262	ATGCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTTGCTCACCTTCC 1321	
Oy Dp	1322	AGAGAGAGTTTTGAGAAGAAGTACTCCGGGAAGGTGGATCCCGGTTCGGAGCCTACG 1381	
oy Op	1382	TTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCCAGCTTCTAATTTTCCCAC 1441	
oy Dp	1442	ACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTACCCGTGC 1501	
Oy Op	1502	TGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCC 1561	
oy Dp	1562	GCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTG 1621 	
oy Ob	1622	TGTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACCCCCATACGGAGCTGTG 1681	
P G	1682	CAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCCTGC	
Qy	1742	ATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCACCTTTC 1801	
٥y	1802	CTGAGGTGTT 1811	

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                           Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y. Method for examining ischemic conditions
Patent: WO 0188188-A 716 22-NOV-2001;
School Juridical Person Nihon University (JP)
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Pred. No. 5.1e-310;
0; Mismatches 217; Indels
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Sequence 716 from Patent WO0188188.
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1. .5841
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Best Local Similarity 87.7%;
Matches 1588; Conservative
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                                                    GCCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCC 1021
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Yoshimura, M. and Cooper, D.M. Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase from NCB-20 cells
ATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTC 1801
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                                         Score 1431.8; DB 10; Length 5841;
Pred. No. 5.1e-310;
0; Mismatches 217; Indels 6;
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adenylyl cyclase; adenylyl cyclase type VI.
Mus.musculus cDNA to mRNA.
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M93422
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oy P	125	TCCCATCCGCATGCGGCTGCCGTCCTCAGCGCCTGGCCTCTCCACCTTGCATTGA 184	
λο	00 (CTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATG 2.	
a	0	TGGCAGCTCAACAGCAGCGACCCCTTCCTTTGGAAGCAGCTCGGTGCTAACG 96	
oy Db	245	IGCIGCIGTICCTCTGCACCAACGICATTAGCAICTGCACACTATCCAGCAGAGGIGT 304	
Qy Db	305	CTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGC 364	
οy	365	TGAGAATCGGCAGCAGGAGCGGCTGCTGTCGGTATTGCCCCCAGCACGTTGCCATGG 424	
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δγ B	602 1327	AGCTGGCTGCGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTG 661 	
δ, O	662	TGTCAGGCTGCCGGAGCCCGACCATGCCCACTGTGTGGAGATGGGGGTAG 721 	
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Oy Dp	1142	CCAAGGACTCCAAGGCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCGGG 1201 	

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                                                                                                       TGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCC 1561
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                                                                                                                                                                    GCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCG 1261
                         ATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTCC
                                                                             TIGCCIGIGCCCIGITGGICITCIGCTICATCTGCTICATCCAGCTICTAATTTTCCCAC
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Search completed: March 1, 2003, 02:24:10 Job time : 3154.21 secs

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1812
1 gttaacgtggtgctgggcat......gcagctttcctgaggtgttc 1812
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
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ALIGNMENTS

RESULT 1 BE840188 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE OFFA	BE840188 676 bp mRNA linear EST 22-SEP-2000 QVO-FN0181-100800-335-d08 FN0181 Homo sapiens cDNA, mRNA sequence. BE840188.1 GI:10272566 EST. human.
REFERENCE	Demonstrates Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 676)
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silvay, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922

Fax: +55-11-2707001

Mon

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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=0V0-FN0181-100 Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 625.
Location/Qualifiers
1. 676
                                                                                                                                                                                                                                                                              /note="Organ: prostate_normal; Vector: puc18; Site_1: Smal site_2: Smal; A mini-library was made by cloning products derived from OMESTERS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Pred. No. 1.5e-131;
0; Mismatches 26;
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Matches 609; Conservative
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1. .581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0999"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196/716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
118 a 157 c 199 g 106 t 1 others
                                                                                                                                                                                                               1 (bases 1 to 581)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                    BG993320 581 bp mRNA linear EST 13-JUN-2001 MR3-HT0999-070201-003-h04 HT0999 Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=MR3&t2=MR3-HT0999-070201-003-h04&t3=2001-02-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 581.
                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
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Catarrhini; Hominidae;
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Pred. No. 8.3e-119;
0; Mismatches 9; 1
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Mammalia; Eutheria; Primates;
                                                                                               GI:14397390
                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
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al Similarity 98.2%;
556; Conservative
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                            sequence tags
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/organism="Mus musculus"
/strain="FYBAN"
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/clone="Insc:4923890"
/clone="Insc:4923890"
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/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: salivary gland; Uector: pCMV-SPORT6; Site_1:
/n
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Mus musculus cDNA clone IMAGE:4923890 5',
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                  1043 AAGAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGC 1102
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov

Tissue procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lettp://mage.lln.gov
Plate: LLAM10845 row: p column: 03
4;
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Pred. No. 2.1e-100;
O; Mismatches 46; Indels
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High quality sequence stop: 565.
Location/Qualifiers
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ilarity 91.2%;
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434 AAGACATCAACACAAAAAAAAGAAGAC---ATGTTCCACAAGATCTACATACAGAAGCATG 490

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovolae; Bovolae; Bovolae; Bos.

1 (bases 1 to 522)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casass, E., Wary, J.E., White, J., Cholae, C.C., Cli., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                    491 ACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCA
                                                                                                               181 CGGAGAATCACTGTCTGAGGATCAAGATCTTAGGAGACTGTTACTACTGCGTGTCTAGGGC
                                                                                                                                                                                                                                                                      TGCCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGTGGAGATGGGGGGTAGACATGATTG
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 48390
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Query Match 23.1%;
Best Local Similarity 77.9%;
Matches 529; Conservative (
                                                                                                                                  pxx-5
                                                                                                                                                          1. .682
                                                                                                                                  Seg primer:
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                                  1. :525
/organism="Bos taurus"
/db_xref=taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."

12 a 162 c 133 g 117 t 1 others
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II HGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507 GTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTGGT
                                                                                                                                                                                                                3;
                                                                                                                                                                                          DB 13; Length 525;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                        Score 442.4; DB 1
Pred. No. 2.2e-95;
0; Mismatches 42
            Seq primer: ATTTAGGTGACACTATAG.
                     Location/Qualifiers
1. .525
Plate: 97 row: A column: 9
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BQ180663.1 GI:20356155
                                                                                                                                                                                        24.4%;
ilarity 91.4%;
Conservative
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Best Local Similarity
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TITLE
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/tissue_tipe="whole brain"
/dev_stage="whole brain"
/dev_stage="whole brain"
/dev_stage="whole Tip phage resistant)"
/lab_host="bull08 (Ti phage resistant)"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, dispeted with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BAAR): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Instututes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."
                                                            CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 CCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACC 205
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                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 418.6; DB 14; Length
Pred. No. 1.2e-89;
0; Mismatches 146; Indels
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/clone="IMAGE:5706065"
/clone_lib="NIH_BMAP_EXO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6"
Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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622

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Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 466)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1905641 EST 30-MAR-2000 CM-BT094-110299-173 BT094 Homo sapiens CDNA, mRNA sequence.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2-CM-BT094-173.html
£t3=110299&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \operatorname{Simpson}, \operatorname{A.J.} Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCGGAGCCTACGTTGCCTGTGCCTGTTGGTCTTCTGCTTCATCTGCTTCATCTAGCT 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1069 CTGCAGCGGACTCGGGCCAACTCCATGGAAGGGC-TGATGCCGCGATGGGTTCCTGATCG 1127
                                                                                                                                          1128 TGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAG 1187
                                                                                                                                                                                                                        1188 CAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCT 1247
                                                                                                                                                                                                                                                                                                     1248 GAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTT 1307
                                                                                                                                                                                                                                                                                                                                                                                   TITGCICACCITCCAGAGAGAGGAITITGAGAAGAAGIACICCCGGAAGGIGGAICCCCG 1367
                                                                                                                                                                                   313
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                                                                                  Gaps
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20202663
                        Indels
    Pred. No. 1.4e-83;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .466
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                      0
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    96.78;
                        412; Conservative
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    Best Local Similarity
Matches 412; Conserv
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//dev_stage="Adult"
//note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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Fax: +55-11-2707001
Enail: asimpsondludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT094-173.html £t3=050299&t4=1)
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1 (Dases I to 442)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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CM-BT094-050299-173 BT094 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="BT094"
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-CM1-FN0105-200
600-280-f02&t3-2000-06-200.td-1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence start: 9
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/db_xref="taxon:9606"
/clone_lib="FN0105"
/dev_stage="Adult"
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1 (bases 1 to 453)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 1.4e-83;
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                                                                                                                                                                                                                                                                                                                                            0; Mismatches
/organism="Homo sapiens"
                                                                                                                                                                                                                            stringency conditions."
                /db_xref="taxon:9606"
/clone_lib="BT094"
/sex="female"
                                                                                                                                                                                                                                          143 g
                                                                                /dev_stage="Adult"
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llarity 96.7%;
Conservative
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BE838164/c
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                               603397792F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5401415 5',
          1333 TTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCC 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapDs-remail.nih.gv
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
Toda Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 638.
Location/Qualifiers
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                                                                                                                                                                      Score 377; DB 13; Length 9
Pred. No. 1.1e-79;
0; Mismatches 160; Indels
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KEYWORDS
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                                                                                                                                                                                                                                                          Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-FNO181-280 700-321-d07&t3=2000-07-28&t4=1) Seq primer: puc 18 forward High quality sequence start: 10 High quality sequence start: 10 High quality sequence stop: 415.
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="FN0181"
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Email: asimpson@ludwig.org.br
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BE840138
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                     Technologies."
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ilarity 98.7%;
Conservative
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BF369868
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AUTHORS
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MEDLINE
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KEYWORDS
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En (bases 1 to 1016)

NHI-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Uppublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Cgapba-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13567 row: f column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT_8229097 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6182035 5', mRNA sequence.
BQ881496
BQ881496.1 GI:22273504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/note="Vector: pcNV-SPORT6 (Life Technologies); Site_1:
Not!; Site_2: Sal!; DNN made by oligo-dr prinning.
Directionally cloned using the following adaptors:
                                                                                                    549
                                                                                                                                                                                                                                                                                                                                          785
252 CAGCAACAGGAGCGTCTCCTGCTGTCTTCCCCTCCATGTTGCCATGGAGATGAAA 311
                                             489
                                                                         371
                                                                                                                    609
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                                                                                                                                                                                                                       699
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                                                                                                                                                                                                                                                                                                             610
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                                                          729 TGAGGCCATCTCGCTGGTACGTGACGTGACAGGTGTGAATGTG---AACATGCGGGTGGG
                                                                                                                                                                                                                                                                                                                                                           GACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGC
                                                                                                                                                               ACTGCGCAGGAGCTGGTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCT
                                                                                                                                                                                                                      GCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGGACTGTTACTACTGTGTGTCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:6182035"
/clone_lib="Lupski_dorsal_root_ganglion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 645.
Location/Qualifiers
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VERSION
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AUTHORS
TITLE
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BQ881496
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 625)

1 (bases I to 625)

1 (bases I to 625)

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., M.J., Soares,F., Bentani,R.R., Bentani,R.R., Tenson,D.F., M.J., Soares,F., M.J., Soares,F., Jongeneel,C.V., O'Hare,M.J., Soares,F., Bentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 24-NOV-2000
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  ö
5'-TCGACCCCACGCTCCG-3' and 5'-TCGACCCCCCT(15)-3'. Size selected > 5'-GACTAGTTCTAGATCGCGAGCGCCCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCTGTGAGGGCCACCATGCCACCT 1792
                                                                                                                                                                                                                                                                                                                                                                                     1433 TTTTCCCACACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTAA 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTGTCCCGCAGCATTGTCCGCTCACGGCACATAGCACCGCAGTTGGCATCTTTTCCG 1612
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20202663
                                                                                                                                                                                                                                                                               Length 1016;
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                                                                                                                                                                                                                                                Score 372; DB 14; I
Pred. No. 1.8e-78;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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BG004182/c
                                                                                         KEYWORDS
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                                                                                                                         Location...

1. .625

/ Corganism="Homo sapiens"

/ Ab_xref="taxon:9606"

/ Alone_lb="GNO1122"

/ Gev_stage="Adult"

/ note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI

/ site_2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent
application No: 196/716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

1.08 a 136 t
This sequence was derived from the FAPESP/LICR Fuman Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-GN0122-259900-424-c07&t3=2000-09-25&t4=1)
Seq primer: puc 18 forward High quality sequence start: 20 High quality sequence stop: 625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 TTACTACTGTGTGTGAGGCTGCCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGGA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 TGTCTCCAATGTTCTCATTTTCTCCTGCACCAACATCGTGGGGTGTCTGCACCCACTATCC 204
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                                                                                                                                                                                                                                                                                                                                                                            Score 361.8; DB 12; Length 625; Pred. No. 4.7e-76; 0; Mismatches 132; Indels 4;
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77.4%;
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RESULT 13

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Location. 1.

1. 611

/ Organism="Homo sapiens"

/ do xerf="texon:9606"

/ clone_lib="GN0122"

/ dev_stage="Adult"

/ dev_stage="Adult"

/ foote="Organ: placenta_normal; Vector: pucl8; Site_l: Smal

/ Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pucl 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                                                                        Dias Neto. E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson(ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-GN0122-201100-555-h12&t3=2000-11-20&t4=1)
Seq primer: puc. Bf forward
High quality sequence start: 7
High quality sequence stop: 611.
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                EST 24-JAN-2001
ысичянв2
QV4-GN0122-201100-555-h12 GN0122 Homo sapiens cbNA, mRNA sequence.
BG004182
                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 611)
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20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Pred. No. 1.5e-72;
0; Mismatches 128
                                                                             BG004182.1 GI:12445098
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Best Local Similarity 77.5%;
Matches 459; Conservative
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Laboratory of Cancer Genetics
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1 (bases I to 673)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2-QV4-GN0122-250900-424-a04&t13-2000-09-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence start: 5
Location/Qualifiers
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
577
                                                                                                                                                 578 ATGAGCTCTTTGCCCGGTTTGACAAGCTGGCGGAGAATCACTGCCTGAGGATCAAAA 637
                                                                                                                                                                                                                        TCTTGGGGGACTGTTACTACTGTGTGAGGGCTGCCGGAGGCCCGGGCCGACCATGCCC 697
                                                                                                                                                                                                                                                                                              518 TTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGA
                                                     --ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACA
                                                                                                                                                                                                                                                                                                                                                    ACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCCATCTCGCTGGTACG 749
                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0122"
/dev_stage="Adult"
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TITLE

FEATURES

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BE001572 367 bp mRNA linear EST 05-JUN-2000 PM2-BN0080-180400-004-g02 BN0080 Homo sapiens cDNA, mRNA sequence. BE001572
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1 (bases I to 367)

1 bolss Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Slmpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                    350 TCCCCGTCATGTTGCCATGGAGATGAAAGCAGACATCAACGCCCAAGCAGGAGGATATGAT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 CCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTG 224
                                                                                                                                                                                                                                                                                                                                                   225 GAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAACGTCATTAGCATCTGCAC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 ACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTACATCCA 344
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20202663
                                                                                                                Length
under low stringency conditions
                                                                                                            Score 345.8; DB 14; Length
Pred. No. 3.3e-72;
0; Mismatches 132; Indels
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                                                                                                            19.18;
76.48;
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM2-BN0080-180 400-004-g02&t3=2000-04-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence start: 15
High quality sequence stop: 367.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nuc	nucleic search, using sw model	
Run on:	February 28, 2003, 21:13:01; Search time 6093.65 Seconds (without alignments) 16949.756 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-750-240-5 :: 3549 1 atgtcatggtttagtggcctaagggaccaaggtgggcact 3549	
Scoring table:	:: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched:	2054640 segs, 14551402878 residues	
Total number of	Total number of hits satisfying chosen parameters: 4109280	
Minimum DB seq 1 Maximum DB seq 1	g length: 0 g length: 2000000000	
Post-processing:	ng: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	GenEmbl:* 1: 9b_ba:* 2: 9b_ha:* 3: 9b_htg:* 4: 9b_om:* 5: 9b_ov:* 6: 9b_pat:* 7: 9b_pat:* 10: 9b_ro:* 11: 9b_vi:* 12: 9b_vi:* 13: 9b_vi:* 14: 9b_vi:* 15: em_hum:* 15: em_lum:* 16: em_lum:* 17: em_lum:* 18: em_li:* 19: em_lum:* 20: em_ow:* 21: em_ov:* 22: em_ov:* 23: em_ov:* 24: em_ph:*	

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Pred. No. is the number of results predicted by chance to have a

AR174473 Sequence
AX189766 Sequence
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AX189768 Sequence
AB007882 Homo sapi
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AX305965 Sequence
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M94422 Mouse adeny
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AX457035 Sequence AX457033 Sequence AX457034 Sequence AB028983 Homo sapi score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. MUSADCYC
AR106659
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MUSADNLCYC SUMMARIES AR174473 AX189761 AX189766 AF250226 AX189768 AB007882 DOGADENCYC IZ9958 AX305965 AR174472 AX189759 DOGADNCYC OCMRADCYV RATADCYA AR106658 AF497517 AC117498 AC021647 AX418303 AC02557 AK093840 DOGADCYC AC074028 BTAC11MR AX107094 AF497516 AX457036 HSADENCYR 10 6 6 10 10 6 10 10 DB 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 77.9 78.1 77.9 78.1 Query Match Length 3549 3484.8 3478.4 3179.2 3156.8 2996.8 296.8 2765 1808.4 1808.4 1691.2 1678.8 1655.2 1648.2 1475.4 1431.6 854.6 842.6 841.8 806.6 597.4 595 Result No.

ALIGNMENTS

RESULT 1

AR174473						
rocus	AR174473	3549 bp	DNA	linear	PAT 1	PAT 17-DEC-2001
DEFINITION	Sequence 5 from patent US 6306830.	S 6306830.				
ACCESSION	ARI74473					
VERSION	AR174473.1 GI:17914793					
KEYWORDS	٠					
SOURCE	Unknown.					
ORGANISM	Unknown.					
	Unclassified.					
REFERENCE	1 (bases 1 to 3549)					
AUTHORS	Hammond, H. Kirk., Insel, P.A., Ping, P., Post, S.R. and Gao, M.	.A., Ping,	Post,	S.R. and	Gao, M	
TITLE	Gene therapy for congestive heart failure	ive heart	failure			
JOURNAL	Patent: US 6306830-A 5 2	3-0CT-2001				
FEATURES	Location/Qualifiers	iers				

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Eukaryota, Metazoa; Chordata; Craniat
Bukaryota, Metazoa; Primates; Catarri
1 (bases 1 to 3549)
Hammond, H.K. and Gao, M.
Gene therapy for congestive heart fai
Patent: Wo 0148164-A 5 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALI
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1025 c 1061 g 764
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CAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG	AGAGCAGCCTGACGCTGCTGGT 	reccecceccttregreegectrategreegetgraacee 60	CGGGGGCGCTTTCGCAGCAGCCCGCGCAGCCCCTCTGCGGGGCCTCTGG 72		TCGGTGCCAATGTGCTGTTCCTCTGCTGTGCCCCAGGCGCAGGCCTTTCAGGCGCAGGCCTTTCAGGCGCAGGCCTTTCAGGCGCAGGCCTTTCAGCGCAGGCCTTTCAGCGCAGGCCTTTCAGCGCAGGCCTTTCAGCGCAGGCCGTTTCAGCGCAGGCCGTTTCAGCGCAGGCAG	ACCCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGCGGG 102 CTGCTGCTGCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGAATCAACAC 108	AAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATCCTG 11	GACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTG
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0y 2 0b 2 0y 3 0y 3		0y 6 0y 6	0y 6 Db 6 Oy 7				Oy 108 Db 108 Oy 114 Db 114	Oy 12 Db 12 Oy 12 Oy 12

9. 0.	1321	GACCATGCCCACTGCTGTGTGGATGGGGGTAGATGATTGAGGCCATCTCGCTGGTA 1380
Qy	1381	CGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAG
Oy Dp	1441	TGCGGCGTCCTTGGCTTGCGAAATGGCAGTTCGATGTGTGGGTCCAATGATGTGACCCTG 1500
Qy Dp	1501	GCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACACTG 1560
oy Op	1561	CAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCGTAC 1620
Qy Db	1621 1621	CTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGCGCCAGCCA
Qy	1681	GAGAAAGGCATGCTGGCCAAGCTGCAGGGACTCGGGCCAACTCCATGGAAGGGCTGATG 1740
Oy Dp	1741	ōō
Qy Dp	1801	GCAAAGACAACC
Qy Db	1861	CTGAGCCGTGCCATCGATGCCCGCAGCAT
Qy	1921	TTTTGCTCACCTTCCAGAGAGA
Qy	1981	AAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTCTGC 2
Qy	2041	AGCTTCTAATTTTCCACACACTCCACCTG
Qy	2101	TGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGTGGT 216
Qy Db	2161	CCCTGCAACGTCTGTCCGCAGCATTGTCCGCTCACGGGCACAT 222
Oy Db	2221	GCAGTIGGCATCTTTCCGTCCTGCTTGTGTTTACTTCTGCCATGCCAACATG 228
Oy Dp	2281	TGTAACCACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACCT 234
Oy Db	2341	CACTGCCTGCCACTGCAGCAGCTCAATTAC
λō	. 0	IGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTG 246

Db 3481 CTCAATGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACCAAG 3540 Qy 3541 GTGGGCACT 3549 Db 3541 GTGGGCACT 3549	3 66 TION ION N DS	human. Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Primates; Catarrhini; Homi 1 (bases 1 to 3552) Hammond, H.K. and Gao, M. Gene therapy for congestive heart failure Patent: WO 0148164-A 10 05-JUL-2001;	OF THE UNIVERSITY OF CALIFORNIA (US) cation/Qualifiers .3552 cganism="Homo sapiens" 2.xref="taxon:9606" 1037 c 1068 g 761 t	Query Match	Oy 61 GAAGGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTGGGCAGGTGGCTTCTGCACG 120	QY 121 CCCGGCTATATGAGCTCCGGGATGCAGACCACCCAGCCCCAGCGCGGGCCC 180	Qy 241 GAGTGGGGCTGCGGGCATGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACG 300 Db 241 GAGTGGGGCTGCGGGCATGGCCCTGGGCTTCGAGGATACCGAGTGACAACGAGGG 300 Qy 301 GGCGGGACGGCTGAGGCCCCGACGGGTGCCCAGGAGTGGCGCGCGC		QY 421 CAGCGGTACTTTTCCAGATGAACCAGGCGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	Qy 541 GTGGCACTGTTGGCCTGTGCCGCCCCCTGTTCGTGGGCCTCATGGTGGTGTGTAACCGG 600 bb 541 GTGGCACTGTTGGCCTGTGCCGCCCCTGTTCGTGGGGCTCATGGTGTGTAACCGG 600
	QY 2521 ATCTITGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATC 2580		OY 2761 CTAAACTTCCTCTGGAAACTACAGGGAAAAAAGAGGAGATGGAGGGGTACAG 2820	OY 2881 GCCGGGAGCGCGCAATGATGAACTCTACTATCAGTGGTGTGTGT	2941 IIIGCLICCATIGCCAACHTICIGAATICATGIGGACTGGAGGCAAGAACATGAG 3001 GCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGTCGACTTTGATGAGATTATCAGG 3001 GCCGAGTGCCTGGCTGGTCAACGAGAGTATCATCGTGACTTTGATGAGATAATCAGG	3061 GAGCGGTTCCGGCAGCTGGAAAGATCAAGACGATGGTGGCACCTACATGCTGCTCCTCA 	3121 GGGCTGAACGCCAGCACCTACGATGGGCCGCTCCCACATCACTGCCCTGAC 3181 TACGCCATGCGCCTCATGGAGCAGATGACACATCAATGAGCACTCTTCAACAATTTC	Oy 3241 CAGATCAAGATTGGGCCCAATCGTGGCAGTGTATCGGGCTCGGAG 3300 1 1 1 1 1 1 1 1 1	3361 GTCCCCGACCGAATCCAGGTGACCGGACCTGTACCAGGTTCTAGCTGCCAAGGGCTAC	

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601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTAACGTGGTGCTGGGCATCCTGGCG 6 [781 GTCCTCGGGGCCTCCTCCCTTGGATTGGATTTGGATTTAGCGT 84 11	QY 961 ACCGCAGTTACATCCAGCCCGGCTCCACCTGCAGCAGGAGAATCGGCAGGAGCGG 1020 Db 111111111111111111111111111111111111	138 CTGTTGCAGACATTGAGGGCTTCACCAGCATCCAGTGCACTGCAGGGGCTG 119	1318 GCGACCATGCCCATGTGGGGGTACATGATGATGATCATCCTCGTG	OY 1558 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCTAGGCCGTGGTGGCAACGC 1617 Db 1561 CTGCAGTACCTGAACGGGGACTACGAGCCAGGCCGTGGTGGCGGAGCGCAACGC 1620 QY 1618 TACCTCAAGGAGCACTTGCTTCCTCATCCTGGGGCCCAGCCAG
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Qy	1678	GAGGAGAAAGGCAIGCIGGCCAAGCIGCAGCGGACTCGGGCCAACTCCAIGGAAGGCTG 1737
Qy	1738	ATGCCGCATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC 1797
Qy Db	1798	CAGATGGGCATTGATGATTCCAGCAAAGACAGGGGCACCCAAGATGCCCTGAACCT 1857
QY	1858 1861	GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG 1917
Qy	1918 1921	CGGAAGGACCAIGIGCGCCGGTTTTTGCTCACCTTCCAGAGAGATTTTGAGAAGAAG 1977
Qy	1978 1981	TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC 2037
QY	2038	IGCITCAICTGCTTCAICCAGCITCTAATITICCCACACTCCACCCTGAIGCTTGGGAIT 2097
Qy	2098	GCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT 2
Qy Db	2158	SCAACGTCTGTCC
Qy Db	2218	ACCGCAGTTGGCATCT ACCGCAGTTGGCATCT
Qy	2278	VACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA 233
oy do	2338	rcrcrgggccrggargcr 239
QV QD	2398	FGTGFGAGGCACCATGCCACTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG 245
Qy	2458	ATC
Qy	2518 2521	5 - 5
Qy	2578 2581	ACAACTATGACCTACTGCTTGGCGTCCATGGC
Qy Db	2638	ACTGTCCAGCTGCAGGAGGGTGGCCCTCAAATATA
Qy Dp	2698	CTGCTGGTGTTTGCGCTGGTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC
Οy		CCTAAACTTCCTCTGGAAACTACAGGCAACAGGGGAAAAAA

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KTIGSTYMAASGLNASTYDQVGRSHITALADYAMRLMEQMKHINEHSFNNFQMKIGLN
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                                     To (bases 1 to 6463)
Wicker, R., Gascon Catalan, A., Cailleux, A.-F., Starenki, D., Stengel, D., Sarasin, A. and Suarez, H.G.
Stengel, D., Sarasin, A. and Suarez, H.G.
Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France Location/Qualifiers
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/product="adenylyl cyclase
/protein_id="AAF82478.1"
/db_xref="GI:9049783"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                                                                                    /tissue_type="thyroid"
complement(19. .447)
'rpt_family="Alu"
/rpt_type=dispersed
469. .561
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Wicker,R., Catalan,A.G., Cailleux,A., Starenki,D., Stengel,D., Sarasin,A. and Suarez,H.G.
Cloning and expression of human adenylyl cyclase type VI in normal thyroid tissues
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GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCCATCCACAGCGGGCGCGTG CTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA 2375 GAGGAGAAGGCCATGCTGCCAAGCTGCAGGGGACTCGGGCCAACTCCATGGAAGGGCTG 2675 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCTGTTGGTCTTC CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCG ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC 2735 TGCTTCATCTGCTTCATCAGCTTCTCATCTTCCCACACTCCACCCTGATGCTTGGGATC ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA GAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG 2495 CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCCAAGATGGCCCTGAACCCT TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA 1798 CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGGCACCCAAGATGCCCTGAACCCT TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC TATGCCAGCATCTTCCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG Oy Dp Qy Db a Sy Op 0y 0b 0y Qy Db Dp ò 셤 οy ద Qγ g Qγ g οy g

08-AUG-2001

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Hammond, H.K. and Gao, M.
Gene therapy for congestive heart failure
patent: W0 0148164-A 12 05-JUL-2001,
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
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AGGACTCCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TAGCTTCCGCCAGGACTCCATGGGTGG AGTGCAGGTCGCAGGGCGCTTTCGCAGCAGAGAGCTGCTGGGTGGG
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2157 1818 1857 1878 1917 1938 1977 1998 2037 2058 2097 2118 2178 2217 2238 2298 2337 2358 2418 2457 2478 2517 2538 2577 2598 2637 2658 2718 2757 2778 2277 2397 2697 11159 ATGCCCGCTGGGTTCCTGACCGTGCCTTCTCCCGGACCAAGGACTCTAAGGCATTCCGC TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCTGATGCTTGGGATT 2059 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCCTGATGCTTGGGATC 2458 CIGCIGAGICITIGGCCAGCICIGICTICCIGCACAICAGCAICGGGAAGIIGGCC ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC 2098 TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT 2359 CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCT CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG 2419 CCCCTGTGTGAGGCACCATGCCCACCTGCACTTTCCTGATCTTCATCGGGAACATG GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA 2179 GGTTCTCTGTTCCCTAAAGGCCCTGCAACGTCTGTCCCGCAGCATGTCCGCTCACGGGCA 2479 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCATCAGCAGCATCGGGAAGTTGGCC CAGATGGGCATTGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT 2278 ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA CCTGCTGACATCACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCT 2578 2599 1858 1879 2038 2158 2338 2398 2659 1738 1819 2638 Q g DP OY DP g g qq ò οy δ δ δ Qγ δ q ò g

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Direct Submission

Direct Submission

Submitted (06-0cT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Submitted (06-0cT-1997) Are 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)

On May 9, 2002 this sequence version replaced gi:2887418.

Sequence updated (05-Jan-1998).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                               /tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
/clone_lib="pBluescriptII SK plus"
/note="This sequence was obtained by subcloning of the DNA fragments derived from two cDNA clones (1 - 1352 was derived from pg00161 and 1353 - 5877 was derived from
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Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
VIII. 78 new cDNA clones from brain which code for large proteins
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SCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG CCCTAAGGCCCTGCAACGTCTGTCCGCAGCATTGTCGCTCACGGGCA GGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG CCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGTGTCCAATGATGAGACC CATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA GAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCG SGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC GGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG TGTGCGCCGGTTTTTGCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAG GGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC CTTCATCCAGCTTCTAATTTTCCCACACTCCACCTGATGCTTGGGATT CCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA AGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC TAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA CACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCT TGATGATTCCAGCAAAGACAACCGGGGCCACCCAAGATGCCCTGAACCCT

Qy 3538 AAGGTGGGCACT 3549 	RESULT 7 DOGADENCYC LOCUS DOGADENCYC LOCUS DEFINITION Canis familiaris adenylyl cyclase type VI mRNA sequence. ACCESSION M94968 VERSION M94968.1 KEYWORDS AGGESTATOR M94968.1 KEYWORDS AGGESTATOR M94968.1 KEYWORDS AGGESTATOR M94968.1 M94968.1	M. S.	AUTHORS Katsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Halnon,N.J., Homoy,C.J. and Ishikawa,Y. TITLE Cloning and characterization of a sixth adenylyl cyclase isoform: types V and VI constitute a subgroup within the mammalian adenylyl	Cyclase family JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992) MEDLINE 92409599	φ.	Aud. Artial Lipeanoisons (Artial Lipeanoisons) (Artial Lipeanoison	Query Match 84.4%; Score 2996.8; DB 4; Length 4046; Best Local Similarity 91.0%; Pred. No. 0; Matches 3233; Conservative 0; Mismatches 307; Indels 12; Gaps 4;	QY 1 AIGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60	Qy 61 GAACGCAATGGGCAGAAGCGTTCGCGGCCCCGTGGCACCTGGGCAGTTCTGCACG 120	QY 121 CCCCGGTATATGAGCTGCCTCCGGGATGCAGACCACCCAGCCCACCCTGCGGGCCCC 180	Oy 181 CCTCGGTGCCCCTGGCAGGTGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGCCAAG 240	Oy 241 GAGCTGGGGCTGCGGGCAGTGGCCTTGGAGATACCGAGGTGACAACGACAGCG 300	QY 301 GGCGGGACGGCTGAGGTGCCCGACGCGTGCCCAGGAGTGGGCGATCTGCTGCCGCGC 360 1 1 1 1 1 1 1 1 1	Qy 361 CGTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTCGGTTCG	Qy 421 CAGCGGTACTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGGTGGTGGTG 480	QY 481 CTGCTCACAGCGGTGCTGCTTCCAAGCCGCCCCGCCCTCAGCCTGT 540
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Q Dp	541	GIGGCACTGTIGGCCIGTGCCGCCCCTGTICGTGGGGCTCATGGTGTGTGTAACCGG 600
Qy Db	601	CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAACGTGGTGGTGGTGCTGCGCG 60
Qy Db	661 785	GCAGTGCAGGTCGGGGGCGCTTTCGCAGCAGACCCGCGCAGCCCCTCTGCGGGCCTCTGG 720
Qy	721	TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCATCCGCATGCGGCTGCC 780
Qy	781	GTCCTCAGCGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT 840
Qy Dp	841 965	GGTGARGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGCTCTCTGCACCAAC 900
Oy Dp	901	GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 960
Oy Dp	961 1085	ACCCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGGGAATCGGCAGCAGGAGGGG 1020
Qy Db	1021	CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGAGAGATGAAAGAAGACATCAACACA 1080
QY Dp	1081	AAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1137
Oy Dp	1138	CTGTTTGCAGACATTGAGGGCTTCACCAGCCAGCATGCAGTGCACGGCGGGGGGCTG 1197
Qy Dp	1198	GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTG
Qy	1258 1385	CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCG 1317
δy	1318	GCCGACCATGCCCACTGCTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1377
Qy Dp	1378	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG 1437
Oy Dp	1438	CACTGCGGCGTCCTTGGCTTGCGGAAATGGCAGTTCGATGGTGGTCCAATGATGTGACC 1497
Qy Db	1498	CTGGCCAACCACGGAAGCAGGAAGCCGGCTGGCCGCATCCACTCGGGCAACA 1557
Oy Op	1558	CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCG 1617

1677 1737 1861 1797 1921 1857 1981 1917 2041 1977 2101 2037 2161 2097 2221 2157 2217 2341 2277 2401 2337 2461 2397 2521 2457 2581 2517 2641 2577 2637 2761 2697 2821 2757 2281 2701 GAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG CAGATGGGCATTGATTCCAGCAAAGACAAACCGGGGCCACCCAAGATGCCCTGAACCCT GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG TITGATGGGCTGGACTGCCCAGCTGCGGGGGGGCTGCACTGAATACATGACCCCTGTG ATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCT CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCC 1618 1742 1862 1858 1918 2042 2102 2162 2282 2518 2698 1678 1802 1738 1798 1922 1982 1978 2038 2098 2222 2158 2218 2342 2278 2402 2462 2522 2582 2578 2702 2762 2338 2398 2458 2642 2638 ð q Q g QΥ Db Qγ ΩD ÓΫ Ω oy D oy D QΥ Dβ oy oy da Qy D Qy Db δ Dp Qy Db δy Ob δŽ δy qq qq g οy δ 4,

JOURNAL Patent: US 5578481-A 1 26-NOV-1996; FEATURES Location/Qualifiers Source 1. 4046 /organism="unknown" BASE COUNT 743 a 1202 c 1257 g 844 t	Query Match 84.3%; Score 2990.4; DB 6; Length 4046; Best Local Similarity 90.9%; Pred. No. 0; Matches 3229; Conservative 0; Mismatches 311; Indels 12; Gaps 4	Qy 1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60	Qy 61 GAACGCAATGGGCAGAAGCGTTCGCGGCACCTCGGGCAGGTGGCTTCTGCACG 120	OY 121 CCCGCTATATGAGCTGCCTCCGGGATGCCAGCCCACCCCACCCCTGCGGGCCC 180	QY 181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGGGGCCCAGGCAAGGCAAG 240	Qy 241 GAGCTGGGGCTGCGCCAGTGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACGG 300	QY 301 GGCGGACGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGCGATCCTGCTGGCGC 360	Oy 361 CGTTIGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC 420	QY 421 CAGCGGTACTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGTG 480	OY 481 CTGCTCACAGGGTGCTGCTTTCCAAGCGGCCCCCCGCCCTCAGCCTGTT 540	Oy 541 GIGGCACTGTTGCCGCCGCCCCGCTGTTCGTGGGCCTCATGGTGGTGTGTAACCGG 600	Oy 601 CATAGCTTCCGCCAGGACTCCATGTGGGTGAGTAACGTGGTGGTGGGGCATCCTGGCG 660 	Qy 661 GCAGTGCAGGTCGGGGGCGCTTTCGCAGCACCCGCGCCCACTCTGCGGCCTCTGG 720	Oy 721 IGCCCIGIGITCTITGTALACAICGCATACACGCTCCTCCCCATCCGCATGCGGGCTGCC 780	Oy 781 GTCCTCAGCGCCTGGGCCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT 840	QY 841 GGTGATGCCTTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAAC 900	Qy 901 GTCATTAGCATCTGCACACTATCCAGCAGGTGTCTCAGGCCAGGCCTTTCAGGAG 960
	QY 2818 CAGGCATACAACCGGAGGTGCTGCATACATTCTGCCCAAGGACGTGGCGGCCCACTTC 2877	QY 2878 CTGGCCCGGGAGCGCCCCAATGATGAACTCTACTATCAGTCGTGAGTGTGTGCGTGTT 2937	QY 2938 AIGTIGCCTCCAITGCCAACTICTCTGAGTICTATGTGGAGGTGGAGGCAAAAATGAG 2997	QY 2998 GGTGCCGAGTGCCTGCGCCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3057	QY 3058 GAGGACCGGTTCCGGCAGCTGGAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3117	OY 3118 TCAGGGCTGAACGCACCACCACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3177	QY 3178 GACTACGCCATGCGGGTCATGGAGCACATGAAGCACATGAAGCACTCCTTCAACAAT 3237	QY 3238 TTCCAGATGAAGATTGGGCTGAACATGGCCCCAGTCGTGGCAGTGTCATCGGGGCTCGG 3297	QY 3298 AAGCCACAGTATGACATCTGGGGGAACACAGTGATGTCTCTAGTCGTATGGACAGCACG 3357	QY 3358 GGGTCCCCAACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3417	QY 3418 TACCAGCTGGAGTGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3477 DD 3542 TACCAGCTGGAGTGTCGAGGGTGAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3601	OY 3478 ITCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCACAAATTCAGCTGAAGGGACC 3537	Qy 3538 AAGGTGGCACT 3549 Db 3662 AAGGTGGCATT 3673	E 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ITION Sequence 1 from patent US 5578481. SION 129958.1 GI:1820749	Unknown. I Unknown. Unclassified	KEFEKENCE I (Dases I to 4046) AUTHORS Ishikawa,Y. TITLE Cloning and characterization of a cardiac adenylyl cyclase

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2758 CGCCTAAACTTCCTCTGGAAACTACAGGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTA 2817 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATGCCAAC GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG 2582 CTGCTGAGTCTCTTGGCCAGCTCTGTTTCCTGCACATCAGTAGCATCGGGAAGTTGGCC ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCC GGTGCCGAGTGCCTGCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC GGTGTCGAGTGCCTGCGGGCTGCTCAACGAAATCATCGCCGACTTTGATGAGATCATCAGC CTGCTGAGTCTCTTGGCCCAGCTCTTCCTTGCACCATCAGCAGCATCGGGAAGTTGGCC 2642 ATGATCTTTGTCCTGGGGGTCATTATTTGGTGCTGCTTCTGCTGGTGGCCCCCCCAGCACC 2698 ATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC 2818 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCAACTTC ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT TITGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC g 90 90 90 03 04 05 05 05 OY OY Db Óλ Q Qγ g δy Db Óλ qq g

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Db 1	1350 CTGAGGATCAAGATCTTAGGAGACTGTTACTACTGCGTGTCAGGGCTGCCCGAGGCCCGG	1409
0y 1	318 GCCGACCATGCCCACTGTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCT	-
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0y 1	1378 GTACGTGAGGTGACAGGTGTGAAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG	1437 1529
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п п	618 TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCAGAACGGAAA 1	67
Qy 1 Db 1	678 GAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG 	1737 1826
0y 1	1738 ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC	1797 1886
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7	1858 GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG	1917 2006
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Oy 1 Db 2	1978 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTC 1 1 1 1 1 1 1 1 1	2037 2126
0y 2	1038 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT	2097 2186
Oy 2	098 TATGCCAGCATCTTCCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT	2157 2246
Oy 2:	158 GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATGTCGGCTCACGGGCA 	2217 2306
Oy 2:	218 CATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC	2277 2366
Oy 2:	278 ATGTTCACCTGTAACCACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA	2337 2426
Oy 2.	338 CCTGCTGACATCACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCT 	2397 2486

2517 2577 3417 2546 2637 2846 2817 2877 3146 3177 3237 2457 2606 2666 2726 2697 2786 2757 2906 2966 2937 3026 2997 3086 3057 3117 3206 3386 3357 3477 3566 CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG ATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAAGAG GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC GAGGAGCGGTTCCGGCAGCTGGAAAAATCAAGACGATTGGTAGCACCTACATGGCTGCC TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTAGTCGTATGGACAGCACG 2487 2518 2667 3087 2398 2458 2547 2607 2578 2638 2727 2698 2787 2758 2847 2818 2907 2878 2967 2938 3027 2998 3058 3147 3118 3207 3178 3267 3238 3298 3387 3358 3327 3447 3418 3507 g οy QQ δλ g QY Db QQ Dp οy g δý g οy qq δ g δy q δy qq δy qq δy a 셤 q q 임 g ò ŏ δ δy δ

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Yoshimura, M. and Cooper, D. M. Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase From NCB-20 cells
Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GAACGCAATGGGCAGAAGCGTTCGCGGCCCGTGGCACTCGGGCAGGGGCTTCTGCACG 120
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         TTCCTCAATGGGGGCCCCCAGCAGTTAACAGGGCCCAGCCAC-AAATTCAGCTGAAGGGAC
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                                                                                MUSADCYC 5841 bp mRNA linear Mouse adenylyl cyclase type VI mRNA, complete cds. M93422
                                                                                                     M93422.1 GI:191690
adenylyl cyclase; adenylyl cyclase type VI.
Mus musculus CDNA to mRNA.
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87.1%; Pred. No. 0;

    .5841
    /organism="Mus musculus"

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                                                                    CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCCAGGCAAGGGCAAG
                                                                                       273 ACTCGGTGCCCTGGCAGGATGAAGCCTTCATCATCAGGAGGGGGGGCCGGGCAGGGTGTG
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GTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTG		CTGGCTAACCACATGGAGGCCGGGGGC GGCCGGCGCATCCACATCACTCGGGC CTGCAGTACTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAA [GAGGAGAAAGGCATGCTGCCAAGCTGCAGCGACTCGGGCCAACTCCATGGAA	CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGCACC [CGGAAGGACCATGTGCGCCGGTTTTGCTCACCTTCCAGAGAGATTTTGAGAAGAGGT	### TROPTCATCTGCTTCTAATTTTCCCACACTCCACCTGATGCTTGGGATT	GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA [
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GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCC CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC CTGGCCCGGGAGCGCCGCAATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGCCAAACAATGAG GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAAFTACTCTCTGGGCCTGGATGCT CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC ATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGG AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTAGTCGTATGGACAGCACG В Q Q B Oy Db Oy Db Qy Dp QY Db OY Db 09 09 qq δy g δ Oy Db Ωp Óγ δy Ω οy 음 Qγ g ò q ò

3447 GGAGTTCCTGACCGAATACAGGTGACTACGGACCTATACCAGGTTCTAGCTGCCAAGGGC 3506	qa	530 CTCCTCATGGCTGTACTGTTGACCTTCCACGCCGCGCCTGCCT
TACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGGGAGATGACCACCTAC 3477 	Qy	541 GTGGCACTGTTGGCCGCCCGCCCTGTTCGTGGGGCTCATGGTGGTGTAACCGG 600
TTCCTCAATGGGGCCCCAGCAGTTAACAGGGCCCAGCCAC-AAATTCAGCTGAAGGGAC 3536 	QQ	601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTAACGTGGTGCTGGGGCATCCTGGCG 660
CAAGGTGGGCACT 3549 	QY	661 GCAGTGCAGGTCGGGGGCGTTTCGCAGCAGCCCGGGCAGCCCTCTGCGGGCCTTGG 720
AR106659 4131 hv naa 1800s nam 14-5555-2001	QY	721 TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCATCCGCATGCGGGCTGCC 780
11 from patent US 6107076.	Qy	781 GTCCTCAGGGGCTGGGGCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT 840
Unknown. Unknown. Unclassified.	Qy	841 GGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCCAATGTGCTGCTGTTCCTCTGCACCAAC 900
Tang.WJ. and Gilman, A.G. Soluble mammalian adenylyl cyclase and uses therefor Patent: US 610707-6-A 11 22-Aug-2000;	Qy	901 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 960
e 14131 /organism="unknown" 835 a 1190 c 1182 g 924 t	Oy Dp	961 ACCCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCG 1020
	Qy	1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAAGGAA
CARGETITAGEGCCTCCTGGTCCTAAAGTGGATGAACGGAAAACAGCCAAAACAGCCAAAACAGCCCTAAAGTTAAAGTTAAACAACGAAAAACAAAAAAAA	da Qy	1081 AAAAAAGAAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1137
GAACGCAATGGACAAAGCGTTCGCGCGCGCGCACTCGGCCAGCTCTCGCACG 120	oy O	1138 CTGTTTGCAGACATTGAGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTG 1197
	Qy Dp	1198 GTCATGACCCTGAATGAGCTCTTTGCCGGTTTGACAAGCTGGCTG
	Qy Dp	1258 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTCAGGGCTGCCGGAGGCCCGG 1317
	Qy Dp	1318 GCCGACCATGCCGCTGTGTGGAGATGGGGGTAGATTGAGGCCATCTCGCTG 1377
36	Qy Dp	1378 GTACGTGAGGTGAGAGTGTGAACATGCGCGTGGGCATCCACAGGGGGCGCGTG 1437
	Qy	1438 CACTGCGGCGTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGGCC 1497
6616	Oy Dp	1498 CTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA 1557
	Oy Db	1558 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCG 1617

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TACCTCAAGGACCAGCACATTGAGACTTTTACCTCCAAGGACCAGCAGCAGTGCACTTGAGACCCTCCAGGAGAGAGA		1618 1 1670 1 1670 1 1730 6 1730 7 17
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RATADCVB

RATALS norvegicus adenylyl cyclase type VI mRNA, complete cds.
M96160.
M96160.1 G1:202718
M96160.1
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RODALNPEDEDVDEFLGRADARSIDQLRKDHYRRFLLTFORDSEDLEKRYRKVDRFG
AYOALLWFCFICTRAPPARALICITYRGIFLLLWYLLCAYCSCGSFPNAL
ORLSRSIVRSRVHSTAVGVFSVLLVFISAIANKFTCSHTPLRTCARMLNLTPSSDVTA
CRLGQLNYSTGLEAPLCEGTARTCSPFEYFVGSYLLGLLASSYFLHISSIGKLVMTY
LGFIYLLLLLLGPPATTFDNYDLLLSVHGLASSNFTPGLLACSAVGATKYMTY
LGFIYLLLLLGPPATTFDNYDLLLSVHGLASSNFTPGLLACSAVGATKYMTY
LVFALALYLHAQQPATTFDNYDLLLSVHGLASSNFTPGLLACPAVGRYALKYMTPVIL
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ISEBRFROLEKIKTIGSTYMAASGLMASTYDOVGRSHITALADYAMRLMEQMHINEH
SENNEQMKICLNMGPVVAGVIGARKPOYDIMGNTVNVSSRMDSTGVPDRIQVTTDLYQ
VLAAKGYGLECRGVYKVKRGEMTTYELNGGPSS"
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                                        Multiple mechanisms underlying desensitization of the liver adenylyl cyclase system. Structure and cAMP regulation of liver adenylyl cyclases
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Premont,R.T., Chen,J., Ma,H.W., Ponnapalli,M. and Iyeng.
Two members of a widely expressed subfamily of hormoneradenyly1 cyclases
Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992) 93028552
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/db_xref="taxon:10116"
/tissue_type="liver, kidney, 1/dev_stage="adult"
                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
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Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.
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Watson,P.A.
3530 TTCCTCAATGGGGGCCCCAGCAGTTAGCAGAGCGCACGAGTGGAAATTCAACCAAAGGGA 3589
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                     181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGGGGCGCCCAGGCAAGGGCAAG
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2337 2532 2592 2652 2517 2712 2772 2637 3012 3312 3177 3372 3432 3492 CACAGCACGGCTGTTGGAGTCTTCTCGGTTCTGCTTGTGTTCATCTCTGCCATTGCCAAC 2472 2397 2457 2577 2832 2697 2892 2757 2952 2817 2877 3072 2937 3132 2997 3192 3057 3252 3117 3237 3297 3357 ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA CTGCTGAGTCTCTTGGCCAGCTCTGTTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC CGCCTAAACTTCCTCTGGAAACTACAGGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTA AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGGTGGAGGCAAACAATGAG TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGG CCTGCTGACATCACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCT GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 2413 2473 2338 2533 2593 2458 2653 2518 2713 2773 2833 2698 2893 2758 2953 2818 3013 2878 3073 3133 3193 3253 3493 2398 2578 2638 2938 2998 3058 3118 3313 3178 3373 3238 3433 3298 QY Db Db Qy g οy g δŻ QQ Oy Oy QQ φ Q δŽ qq Qγ g Qγ q δ qq O. Db QQ Dp οy Db Qy Db δý g Qγ g δ g

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MASSTANFERFRELEANHEYBCIKLLINEITAPDELISEBRROLEKTKTIGSTYM
ARASGLINASYYDOYSENITALADYAMELMEDKKHINBHSFNNFOMKTGLINMGPVVAGY
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YDLLLGVHGLASSNETFDGQDCPAVGRVALKYMTPVILLVFALALYLHAQQVESTARI
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Pred. No. 0;
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HAPARAPQPOPAVALLICASVILEVULWVCNRHSFRQDSWWVSYVVLGILAXVQVGG
ALAANPHSFSAGLWGVPFFVY ITYTLLPIRKRAAVLSGLGISTLHI.ILAWQINSSDP
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SLVREVTGVNVNMRVGIHSGRVHCGVLGLKKWQFDVWSNDYTLANHBAGGRAGRIHAI
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NABGCLMPRWYDRAFSKTROSKAFRQMGIDDSSKDNRGAQDALNPEDEVDEFLGRAI
DARSIDQLAKDHVRFELLTFQREDLERKY STRVDPRFGAYVACALLYFCFICFTQLLV
FPYSTLILGIYAAIFLLLLLVTVLICAVCSCGSFPFKALQRLSRNIYRSRGHSTAVGIF
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partial cds.
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APTCSFPEYFVGNVLLSLLASSVFLHISSIGKLAMTFILGFTYLVLLLLGPPAAIFDN
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2 (bases 1 to 3465)
Premont, R.T., Jacobowitz, O. and Iyengar, R. Lowered responsiveness of the catalyst of adenylyl cyclase to stimulation by GS in heterologous desensitization: a role for adenosine 3',5' amonophosphate-dependent phosphorylation
Endocrinology 131 (6), 2774-2784 (1992)
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                                                                                                                                                   TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGC--CACAAATTCAGCTGAAGGGA 3535
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                                3613 TACCAACTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGGAAAGGGGGAGATGACCCAAC
              GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC
                                                                                TACCAGCTGGAGGGGTGGTCAAGGTGAAGGGCGAAGGGGGGAGATGACCTAC
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Mammalia; Eutheria; Rodentia;
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/citation=[2]
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adenylyl cyclase type VI.
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2175 2295 2355 2415 2214 2334 2394 2475 2454 2535 2514 2595 2574 2715 2775 2835 2895 2634 2694 2754 2814 2874 2994 3135 3054 CAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTG ATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCAC ACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCC TGCCACCTGCAGCAGCTCAATTACTCTTGGGCCTGGATGCTCCCCTGTGTGAGGGCACC ATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTGGCC CTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCCTCTGG **AAACTACAGGCAACAGGGGAAAAAGAGGAGGATGGAGGAGCTACAGGCATACAACCGGAGG** CTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCTCAGGGCTGAACGCCAGC CTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTCCTGGCCCGGGAGCGCCGC AATGATGAACTCTACTATCAGTCGTGTGAGTGTGGGCTGTTATGTTTGCCTCCATTGCC AACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAGGGTGCCGAGTGCCTGCGG CTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAG 1975 2056 2035 2116 2095 2176 2155 2236 2215 2296 2275 2356 2416 2476 2455 2575 2656 2716 2695 2755 2836 2875 2956 2896 2935 3016 3076 2995 g g Qγ 5 G 92 93 93 93 g do oy Db Qy QΩ ΟΥ Db qq ά Qy Db ò g δ qq Qγ qq ò g οy Db ŏ qq ά

303 GTCTCAGCGCCAGGCCTTTCAGGAGCCCGCAGTTACATCCAGGCCCGGCTCCACCTGCA 362	996 GCATGAGAATCGGCAGCAGGAGCGGCTGCTGCTCGGTATTGCCCCAGCACGTTGCCAT 1055	1056 GGAGATGAAAGAAGATCAACACAAAAAAAGAAGACATGTTCCACAAGATCTACATACA	1116 GAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATC 1175	1176 CCAGIGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAA 1235 	1236 GCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGT 1295 	1296 GTCAGGGCTGCCGGAGGCCCGGCCGACCATGCCCACTGCTGTGGGGGATGGGGGTAGA 1355	1356 CATGATTGAGGCCATCTCGCTGGTACGTGACAGGTGACAGTGTGAATGTGAACATGCGCGT 1415 	1416 GGGCATCCACAGCGGGCGCGTGCACCTGCGCTCCTTGCCTTGCGGAAATGGCAGTTCGA 1475	1476 TGTGTGGTCCAATGAGCCTGGCCAACCATGGAAGCAGGAAGCGGGCTGGCCG 1535	1536 CATCCACATCACTCGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGG 1595 	1596 CCGTGGTGGCAAGGGGAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCT 1655	1656 GGGCGCCAGCCAGAAACGGAAAGGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCG 1715	1716 GGCCAACTCCATGGAAGGCTGATGCCGCATGGGTTCCTGATCGTGCCTTCTCCCGGAC 1775	1776 CAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATGATGAGAAGACAACCGGGG 1835	1836 CACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGA 1895 	1896 IGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTCCA 1955	1956 GAGAGAGGATTTTGAGAAGAACTACTCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGT 2015	2016 TGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACA 2075 1363 TGCCTGCTGCTGTTGTTTTGTTGTTGTTGTTGTTGTTGTT
Q	, Qy Db	Qy Db	QY Db	Qy Db	Qy	Qy Up	Qy Db	Qy	Qy	40 AO	QQ Op	QY Db	Oy Ob	Oy Db	QY Db	Qy Db	QY	Qy Db
Db 3055 TTGGAGAAGATCAAGACCATCGGTAGCACCTACATGGCCGCCTCTGGGCTAAATGCCAGC 3114	QY 3136 ACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCTGGCTGACTACGCCATGCGGCTC 3195	OY 3196 ATGGAGCAGATGAACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGG 3255 	QY 3256 CTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGCTCGGAAGCCACAGTATGACATC 3315	QY 3316 TGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCAGGGGTCCCCGACCGA	QY 3376 CAGGTGACCACGGACTGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGAGTGTCGA 3435	OY 3436 GGGGTGGTCAAGGTGAAGGGGGAGATGACCACCTACTTCCTCAA 3485 		DEFINITION Sequence 3 from patent US 6306830. ACCESSION AR174472 VERSION AR174472 GI:17914792	WS L	AUTHORS Hammond, H. Kirk, Insel, P.A., Ping, P., Post, S.R. and Gao, M. TITLE Gene therapy for congestive heart failure JOURNAL Patent: US 63068304 3 23-0CT-2001;	rce	/ Match 51.0%; Score 1808.4; DB 6; Length 1812; Local Smilarity 99.9%; Pred, No. 0; 0; no magnetic of the conservation of the manual state of the conservations of the second of the conservations of the conservations of the second of the conservations of the con	GCATCCTGGCGGCAGTCGGGGGGCGCTTTCGCAGCAGCAGCGGGGGGGCGCTTTCGCAGCAGCAGCAGCGGGGGGGG	696 GCGCAGCCCCTCTGCGGCCTCTGGTGTTCTTTGTATACATCCCCTCTTTTTTTT	756 CCTCCCCATCCGCATGCGGCTGCCGTCCTCAGCGGCCTGGGCCTGCCT	816 GATCTTGGCCTGGCAACTTAACCGTGGTGATCCTTCCTCTGGAAGCAGCTCGGTGAA 87 1	876 TGTGCTGCTCCTCTGCACCACGTCATTAGCATCTCGCACACACA	936 GTCTCAGCGCCAGGCCTTCAGGAGACCCGCAGTTACATCCAGGCCCGGCTCCACTGCA 99

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                                                  1623 GTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGAGCTGTGC 1682
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                                                                                                                                                         TGAGGTGTCC 2445
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TGAGGTGTTC 1812
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Job time: 6121.65 secs
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_	3549	100.0	3549	22	AAD08563	Human cardiac aden
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4	3379.2	95.2	3582	22	AAD08568	Human modified car
J.	2996.8	84.4	4046	14	AAQ42525	Cardiac adenylyl c
9	2765	77.9	5841	24	AB199680	Mouse ischaemic co
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The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ARS) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ARSPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and CAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ARP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present DNR sequence encodes human cardiac adenylcyclase VI (GVCVI) isoform which is used for generating a this deta-ARP transgene, used in the exemplification
                                                                                                                                                      Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure
                                                                                                                                                                                                                                                Example 5; Page 122-129; 153pp; English
(REGC ) UNIV CALIFORNIA
                                            Gao M;
                                                                                       WPI; 2001-418260/44
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240 540 61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120 180 240 GAGCTGGGGCTGCGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300 300 GGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGCGATCCTGCTGGCGC 360 360 420 420 480 600 Gaps 1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGGT 60 9 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGGGGCCCAGGCAAGGGCAAG CGTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC 121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC CAGCGGTACTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGGTGGTGCTGGTG GTGGCACTGTTGGCCTGTGCCGCCCCTGTTCGTGGGGGCTCATGGTGGTGTAACCGG DB 22; Length 3549; Indels ó; 100.0%; Score 3549; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Best Local Similarity Matches 3549; Conserv Query Match 241 181 181 241 301 361 301 361 421 481 481 541 541 421 qq ò qq Q q ò QQ Dp g g ò ò ò ò ò à à à

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Qy Db	661	GCAGTGCAGGTCGGGGCGCTTTCGCAGCAGACCCGCGCAGCCC
Qy Db	721	TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCATCCGCATGCGGGCTGCC 78
oy do	781	GTCCTCAGCGGCCTGG
Qy Db	4 4	GGTGATGCCTTCCTCTGGAAGCACTCGGTGCCAATGTGCTGCTGCTTCCTGCACCAAC 90
Q.y Db	901	GTCATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCCAGGCCTTTCAGGAG 96
QY	961	ACCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAG
Oy Db	1021	CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 108
QY Db	1081	AAAAAAGAAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATCCTG 114
oy ob	1141	TITGCAGACATIGAGGGTICACCAGCCIGGGATCCCAGIGCACIGCGCAGGAGCIGGTC 120
Qy	1201	ATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTG
Oy Dp	1261	AGGATCAAGATCTTGGGGGACTGTTACTACTGTGTCAGGGCTGCCGGAGGCCCGGGCC 132
Qy Db	1321 1321	GACCATGCCCACTGCTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTA 138
Qy Db	1381 1381	CGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGCAC 14
Qy Dp	1441	TGCGGCGTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGGGTCCAATGATGTGACCCTG 150
Oy Dp	1501	GCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACACTG 156
QY Db	1561	CAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCGTAC 162
Qy	1621	AGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAG
δy		SAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGGCCAACTCCATGGAAGGGCTGATG 17

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Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

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qa	oy Dp	oy op	Š A	QY	QY Dp	Qy Dp	Oy Dp	Qy Dp	Qy Db	QQ Dp	Qy Db	Q7 Q0	Q Q	RE AA	K K K E	X X DE	K K K K	XX SO XX
	y 1741 CCGCGATGGGTTCCTGATGGTGCCTTCTCCCGGACCAAGGCCTTCCGCCAG 1800	y 1801 atgggcattgatgatgatgcagcaaagacaaccggggcacccaagatgcctgaaccctgag 1860 	y 1861 GATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGG 1920	1921 AAGGACCATGTGCGCGGTTTTTGCTCACCTTCCAGAGAGAG	y 1981 TCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTTGGTTG	7 2041 TTCATCTGCTTCATCCAGCTTCTAATTTTCCCACCTCCACCCTGATGCTTGGGATTTAT 2100	2101 GCCAGCATCTTCCTGCTGCTGCT 	y 2161 TCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCGCTCACGGGGACAT 2220	2221 AGCACGCAGTTGGCATCTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATG	2281 TTCACCTGTAACCACCCCCATACGGAGCTGTGGAGCCGGGATGCTGAATTTAACACCT 2340	2341 GCTGACATCACTGCCTGCCACCTGCAGCACTCAATTACTCTCTGGGCCTGGATGCTCCC 2	y 2401 CTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTG 2460 	y 2461 CTGAGTCTCTTGGCCAGCTCTGTCTTGCTGCACATCAGCATCGGGAAGTTGGCCATG 2520 	y 2521 ATCTTTGTCTTGGGGCTCATCTATTGGTGCTGCTTCTGGGGTCCCCCAGCGGCGCATC 2580 	y 2581 TITGACAACTATGACCTACTGCTTGGCTCCATGGCTTGGCT	y 2641 GATGGCTGGACTGTCCAGCTGCAGGAGGTGGCCCTCAAATATATGACCCCTGTGATT 2700 	7 2701 CTGCTGGTGTTTGCGCTGGTATCTGCATGCTCAGGTGGAATCGACTGCCCGC 2760 	y 2761 CTAAACTTCCTCTGGAAACTACAGGGAAAAAAAGAGGAGAGTGGAGGAGCTACAG 2820
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ling protein; beta-ASP; ic receptor; beta-AR; syntherase; lsease; congestive heart failure; beta-ASP transgene; ds. GGCAGGTGTCATCGGGGCTCGGAAG 3300 CCACAAATTCAGCTGAAGGGACCAAG 3540 CCAAGGACGTGGCGGCCCACTTCCTG 2880 KGTCGTGTGAGTGTGGCTGTTATG 2940 TGACTTTGATGAGATTATCAGCGAG 3060 TGGTAGCACCTACATGGCTGCCTCA 3120 CCTCCCACATCACTGCCCTGGCTGAC 3180 CCAGGTTCTAGCTGCCAAGGCTAC 3420 AAAAGAGGAGATGGAGGAGCTACAG 2820 CTCTAGTCGTATGGACAGCACGGGG 3360 CAAGGGGGAGATGACCACCTACTTC 3480 oform #2 DNA.

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                                      541 GIGGCACTGTTGGCCTGTGCCGCCCCTGTTCGTGGGGGCTCATGGTGGTGTTAACCGG
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Qy 2578 ATCT Db 2581 ATCT	Oy 2638 TTTG Db 2641 TTTG			Oy 2818 CAGG Db 2821 CAGG	2878	2938	Oy 2998 GGTG Db 3001 GGTG	Oy 3058 GAGG Db 3061 GAGG	3118	Qy 3178 GACT Db 3181 GACT	Qy 3238 TTCC Db 3241 TTCC	Qy 3298 AAGC Db 3301 AAGC		Oy 3418 TACC Db 3421 TACC	Qy 3478 TTCC Db 3481 TTCC	Qy 3538 AAGG Db 3541 AAGG	RESULT 3 AAX00461 ID AAX00461 XX
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ACATCACT	GTGGCAAG	CCAGCCAG	ACTCCATG - - - - - ACTCCATG	ACTCCAAG	AAGATGCC AAGATGCC	GCAGCATT GCAGCATT	AGGATTTT AGGATCTT	GTGCCCTG GTGCCCTG	CCCTGATG	GTGCTGTG 	TTGTCCGC	CTTCTGCC	GGATGCTG, GGATGCTG	CTCTGGGC 	TGTCCATCO ACTTCATO	GCATCGGG GCATCGGG	TGGGTCCC TGGGTCCC
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CTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA 	CTGCAGTRACTGRACGGGACTACGAAGTGGAGCCAGGCCAG	TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGGGCCAGCAGAAACGGAAA 	GAGGAGAAAGGCATGCTGGCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG 	ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC	CAGATGGGCATTGATGATTCCAGCAAAGACAACGGGGGCACCCAAGATGCCCTGAACCT 	GAGGATGAGGTGGATGAGTTCCTGAGCGGTGCCATGCCTGCGGGAGCATGATGATCAGCTC 	CGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTCCAGAGAGGGTTTTTGAGAAGAG 	TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCTGTTGGTCTTG TACTCCCGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCTGTGCCTGTGCTTCTTTTTTTT	TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT	TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTAACTCCTGT 	GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGCAACGTCACGGCAACGTCTCTCTC	CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC	ATGTTCACCTGTAACCACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA 	CCTGCTGACATCACTGCCTGCACCTGCAGCTCAATTACTCTCTGGGGCCTGGATGCT 	CCCCTGTGTGAGGGACCATGCCCACTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG	CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 	ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTTGCTT
1498 CT 1501 CT		1618 TR 1621 TR	1678 GP 	1738 AD 1741 AD	1798 CF 1801 CF	1858 GF 1861 GF	1918 CG 1921 CG	1978 TR		2098 TA 1 1	2158 GG 1158 GG 2161 GG	2218 CA 11 2221 CA	2278 AT 2281 AT	2338 CC 1 2341 CC	2398 CC 2401 CC	2458 CT 2461 CT	2518 AT 2521 AT
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2640 2697 2700 2757 2760 2817 2820 2877 2880 2937 2940 2997 3000 3057 3060 3117 3120 3177 3180 3237 3240 3297 3300 3357 3417 3420 3480 3537 3540 CAGCTGGAGTGTCGAGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3477 TTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCCTACCAATGAGACC 2637 CAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGGGTCTCGGGCTCGGGCTCGGGCTCGGGGCTCGGGGCTCGGGGCTCGGGGCTCGGGGCTCGGGGCTCGGGGCTCGGGGCTCGGGGCTCGGGGGCTCGGGGGCTCGGGGGCTCGGGGGCTCGGGGGCTCGGGGGCTCGG CTAAACTTCCTCTGGAAACTACAGGCAACAGGGGAAAAAGAGGGAGATGGAGGAGCTA GAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC TACGCCATGCGCCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT GTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC GATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG GATGGGCTGGACTGTCCAGCTGCAGGGAGGTGGCCCTCAAATATATGACCCCTGTG TITGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG GCCGAGTGCCTGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC GGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT CCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3552 GIGGCCACT 3549 GIGGGCACT

Db 3541 AAGGTGGCCACT 3552
RESULT 3
AAX00461
LD AAX00461 standard; cDNA; 4942 BP

us-09-750-240-5.rng

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GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGGTGACAACGACAGCG

CGTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC

GGCGGGACGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGCGATCCTGCTGGCGC

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420 564 480 540

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CAGCGGTACTTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGGTGGTGGTGGTGGTG

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GTCCTCAGCGCCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT GTCCTCAGCGGCCTGGGCCTCTCCACCTTGATTGATCTTGGCCTGGCAACTTAAACCGT

TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCCATCCGCATGCGGGCTGCC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA sequence encodes human type VI adenylyl cyclase (hAc6, see AAW30599) that is expressed mainly in the heart and brain. hAc6 has a similar putative structure to other adenylyl cyclase isoforms but, like type V, is distinguishable in that it has a larger region. hAc6 coNA was initially shorter C-terminus as it lacks the C2b region. hAc6 coNA was initially isolated from a human heart cDNA library using an adenylyl cyclase PCR fragment as probe. It was used to design primers that were used in a PCR-based RACE to obtain the full-length cDNA sequence. The invention relates to the hAc6 gene, methods for the recombinant production of purified hAc6 and the proteins made by these methods, antibodies against hAc6, vectors, probes and host cells (especially HEK-293) transformed by cans encoding polypeptides having hAc6 activity, along with diagnostic and therapeutic uses for these various reagents. hAc6 can be used as a tool to screen for agonists and antagonists that in treating diseases caused by aberrant activity of this enzyme, and diseases whose symptoms can be amellorated by stimulating or inhibiting the activity of hAc6.
                                                                                                                                                                                                                                                                                                                                                                            Newly isolated and purified human type VI adenylyl cyclase (hAC6) oblypeptide - useful for identifying potential therapeutic agents that modulate hAC6 activity, and for the diagnosis of hAC6-associated diseases and disorders
                                                                           ds,
                                                                         Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;
                                                Human type VI adenylyl cyclase cDNA.
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 1A-I; 42pp; English.
                                                                                                                                                                                                                                                                                       THERAPEUTICS INC
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P-PSDB; AAW30599.
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AAX00461
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CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACAA 1080 AAAAAAGAAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1137 ||||||||||||||| AAAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1284 1285 CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTG 1344 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCCAGGCCTTTCAGGAG ACCCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTG 1045 1105 1021 1225 961 1081 1138 1165 g ò Dp ò g οy g δy ä CCCCCCTATATGAGCTCCCTCCGGGATGCAGACCACCCAGCCCCACCCCTGCGGGCCCC 180 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCCTGGGCACTCGGGCAGGTGGCTTCTGCACG 120 204 264 Gaps 1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT Length 4942; 3; 36; Indels DB 20; Score 3478.4; Pred. No. 0; 0; Mismatches 98.0%;

Best_Local Similarity 98.9 Matches 3513; Conservative

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Query Match

1020 1164

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Oy 2338 CCTGCTGACATCACTGCCTG Db 2485 CCTGCTGACATCACTGCCTG Oy 2398 CCCCTGTGTGAGGGCACCAT Db 2545 CCCCTGTGTGAGGGCACCAT Oy 2458 CTGCTGTGTGAGGGCACCAT Oy 2458 CTGCTGAGTCTTTGGCCAG Oy 2518 ATGATCTTTGTCTTGGGGCT Oy 2518 ATGATCTTTGTCTTGGGGCT Oy 2578 ATGATCTTTGAGACT OY 2578 ATGATCTTTGACTTTGAGACT OY 2578 ATGATCTTTGACACT OY 2578 ATGATCTTTGACTTTGAGACT OY 2578 ATGATCTTTGACTTTGAGACTTTGACTTTGAGACTTTTGACTTTGAGACTTTTGACTTTTGAGACTTTTGACTTTTGAGACTTTTGACTTTTGAGACTTTTGACTTTTGAGACTTTTGACTTTTTTTT	Db 2725 ATTTTTGAACTATGACT OY 2638 TTTGATGGCTGGACTGTCC Db 2785 TTTGATGGCTGGACTGTCC OY 2698 ATTCTGCTGGTGTTTGCGCT OY 2698 ATTCTGCTGGTGTTTGCGCT OY 2698 ATTCTGCTGGTGTTTGCGCT OY 2758 CGCCTAAACTTCCTCTGGAA OY 2758 CGCCTAAACTTCCTCTGGAA OY 2758 CGCCTAAACTTCCTCTGGAA OY 2758 CGCCTAAACTTCCTCTGGAA OY 2905 CGCCTAAACTTCCTCTGGAA OY 2818 CAGCCATACAACCGGAGGCT Db 2965 CAGGCATACAACCGGAGGCT	OY 2878 CTGGCCGGGAGCGCGCAA Db 3025 CTGGCCCGGGAGCGCCGCAA QY 2938 ATGTTTGCCTCCATTGCCAA QY 2998 GTGTCGCTCCATTGCCAA QY 2998 GTGTCGGTTGCCAT QY 2998 GTGTCGGGTCTCGGCT QY 3058 GAGGAGCGGTCCGGCGCT QY 3058 GAGGAGCGGTCCGGCGCT QY 3118 TCAGGCTTCCGGCAGCTCC	326 332 333 333 344 350 350 350
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CAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGG	1518 CTGCCAACCACATGAAGCGGGCTGGCCGATCCAATCATACATA	Oy 1798 CAGATGGGCATTGATCAGCAAAGACAAGGGGCACCCAAGATCCAAGACTCCGC 1944 Oy 1798 CAGATGGGCATTGATGATCCAGCAAGACAACGGGGCACCCAAGATGCCTGAACCCT 1857 1945 CAGATGGGCATTGATGATCCTGAAGACAACGGGGGACCCCAAGATGATCCTCAACCCT 2004 Oy 1858 GAGGATGAGGATGATCCTCAAGACCTGCATCCATCGATGACCCCTCAACACCTTCAACACCTTCAACACCTTCAACACTTTCATCA	Qy 2038 TGCTTCATCTGCTTCATCTAATTTTCCCACACTCCACCTGATGCATT 2097 Db 2185 TGCTTCATCTGCTTCATCTTCCCACACTCCACCTGATGCTTGGGATC 2244 Qy 2098 TATGCCAGCATCTTCCTGCTTCATCTTCCTGCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT

CCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG 2697 3GGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3477 TGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC ACTICICIGAGITCIAIGIGAGCIGGAGGAACAAIGAG GCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCT GCCACCTGCAGCAGCTCAATTACTCTTGGGGCCTGGATGCT TGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG GCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC TGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC AACTACAGGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTA ACTICICICAGITCIATGIGGAGCIGGAGGCAAACAATGAG TGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC TGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC TGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC CCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT TGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT TGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGG AGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC

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myocardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylytoyclase; adenylytate.oyclase; cAMP synthetase; GAP copertor kinase; GRK; heart disease; congestive heart failure; cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compositions for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present cDNA sequence encodes human modified cardiac adenylcyclase VI (ACVI) isoform which is used for
                                                            Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the exemplification of the
TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiac ACVI isoform"
                                                                                                                                                                                                                                                                                                                                cardiant; beta-adrenergic signalling protein; beta-ASP;
                                                                                                                                                                                                                                                                                                Human modified cardiac adenylcyclase VI (ACVI) isoform cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-ASP transgene, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 143-150; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 22..3525
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                   Indels
                  88;
Score 3379.2;
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95.2%;
97.4%;
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Matches 3458;
Query Match
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		1318 GCCGACCATGCCCACTGCTGTTT	1438 CACTGCGCGTCCTTGGCTTGCG 	1558 CTGCAGTACCTGAACGGGGACTA 	1678 GAGGAGAAAGGCATGCTGGCCAA 	1798 CAGATGGCATTGATGATTCCAG		1999 TACTCCCGGAAGGTGGATCCCCG 2038 TGCTTCATCTGCTTCATCCAGCT 2059 TGCTTCATCTGCTTCATCCAGCT 2098 TATGCCAGCATCTTCCTGCTGCTCTCTTCTTCTTCTTCTTCTTCTTCTTTTTT
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TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTACTCCTGT GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA CCTGCTGACATCACTGCCTGCCACCTGCAGCACCTCAATTACTCTGGGGCCTGGATGCT CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG CTGCTGAGTCTCTTGGCCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC TTTGATGGGCTGGACTGTCCAGCTGCAGGGGGGGGGGCCCTCAAATATATGACCCCTGTG ATTCTGCTGGTGTTTGCGCTGTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC 2758 CGCCTAAACTTCCTCTGGAAACTACAGGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTA CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC 2839 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT GACTACGCCATGCGGCTCATGCAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT

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     GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC
                                                                                                   TACCAGCTGGAGTGTCGAGGGGTGGTGAAGGGCCAAGGGGGGAGATGACCACCTAC
                                                                                                                                   TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC
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                                                                                                                                                                                                                                                                                        heart
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                                                                                                                                                                                                                                                                                       function;
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                                                                                                                                                                                                                                                                      Cardiac adenylyl cyclase gene
                                                                                                                                                                                                                         AAQ42525 standard; DNA; 4046
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                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                  AAGGTGGGCACT 3549
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P-PSDB; AAR37309.
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canine cardiac adenylyl cyclase gene. The gene is suspected of being involved in the regulation of cardiac function and it is thought that decreased activity of adenylyl cyclase in the heart may be a major factor in the development of heart failure. Thus the adenylyl cyclase gene is useful to screen cpds. which stimulate the activity
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                                                                                                                     Length 4046;
                                                                                                                                               12;
                                                                                                                                               Indels
                                                                                          Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;
                                                                                                                     DB 14;
                                                                                                                                             307;
                                                                                                                    Score 2996.8;
Pred. No. 0;
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Similarity 91.0%;
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 2102 TACTCAAGGA 2038 TGCTTCATCT 2162 TGCTTCATCT 2098 TATGCCAGCA 	2158 GGTTCTCTGT 2282 GGCTCTCTCT 2218 CATAGCACCG 1 2342 CACAGCACTG 2278 ATGTTCACCT 2402 ATGTTCACCT		2518 ATGATCTTTG [2698 ATTCTGCTGG 2822 AITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	2878 CTGGCCCGGG 3002 CTGGCCCGGG 2938 ATGTTGCCT 3062 ATGTTGCCT 3062 GTGCCGAGT 2998 GGTGCCGAGT 11111111111111111111111111111111111
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CTCAGCGCCAGGCCTTTCAGGAG	AGCTGGGGGGGGGATCCCCCCCCCCCCCCCCCCCCCCCC	LAGCTGGCTGCGGAAAATCACTGC			GCACCCAAGATGCCCTGAACCCT
GTCATTAGCATCTGCACACACTATCCAGGAGAGTGTCTCAGGGCCCAGGCCTTTCAGGAG	AAAAAGAAGACTCCACAAGATCTACATAGAAGATGAAGAATGAAAAAAAA	GTCATGACCCTGAACGAGCTCTTCGCCCGGTTTGACAAGCTGGCGGAAAATCACTGC CTGAGGATCAAGATCTTGGGGAACTGTTACTACTGTCTCAGGGCTGCCGGAGGCCCGG [GACTGCGGCGTCTTGGCTTGCGAAATGCGCGTGGGCGTTCGAAGGGGGCGTGTG CACTGCGGCGCTCTTGGCTTGG	TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCCA	CAGATGGGCATTGATGATGCAGCAAACGGGGGCACCCAAGATGCCCTGAACCTT
901 GTCATTAGCATCTT 1025 GTCATTGCCATCTT 961 ACCGCAGTTACA' 1011 1111 1085 ACCGCGCGTTACA' 1081 CTGCTGCTGCGG' 1021 CTGCTGCTGCGG'		1325 GTCATGACCTGAJ 1258 CTGAGGATCAAGA 1385 CTGAGGATCAAGA 1318 GCCGACCATGCCCJ 1445 GCAGCCATGCCCJ 1378 GTACGTGAGGTGA		1618 TACCTCAAGGAGCJ 1742 TACCTCAAGGAGCJ 1678 GAGGAGAAAGGCAF 11802 GAGGAGAAAGGCAF 11802 GAGGAGAAGGCAF 1738 ATGCCGCGAAGGGCAF 1738 ATGCCACCTGGGG	8 7 8 7 8 7 8
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TTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3117 ATCTICCTGCTGCTAATCACCGTGCTGATCTGTGTGTGTACTCCTGT TTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA GCAGTTGGCATCTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC GAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG CTCTTGGCCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC GTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCC AACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC CTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG GTGTTTGCGCTGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC AACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC TCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG TGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC

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Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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                   AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse ischaemic condition related cDNA
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P-PSDB; ABB57257.
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The present invention describes a method for examining ischaemic

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genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in AB857020 to AB857374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for a mouse ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
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                                GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                cyclic AMP; adenosine monophosphate; screening; stimulation; inhibition; treatment; cholera; pituitary tumour; heart failure; ischaemia; endocrine disorder; cell necrosis; pseudohypoparathyroidism; endocrine deficiency; human; ss.
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A recombinant Adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzyme which allows easier screening of compounds that stimulate and inhibit Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimera of adenylyl cyclase (1 and C_2 domains linked covalently. The domains may be linked by a linker peptide. The recombinant adenylyl cyclase is useful for screening inhibitors and stimulators of adenylyl cyclase activity. Inhibitors of the enzyme are useful for treating cholera, pitultary tumors, heart failure, ischaemia, endocrine disorders and cell necrosis. Stimulators of adenylyl cyclase are useful for treating pseudohypoparathyroidism and other
                                                                                                                                                                       Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGCCCCAGGCAAGGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 ACTCGGTGCCCCTGGCAGGATGAAGCCTTCATCAGGAGGGCTGGCCGGGAAGGGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCTGGGGCTGCGGCCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGGGACGGCTGAGGTGCCCCCGACGCGGTGCCCAGGAGTGGGCGATCCTGCTGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGCACTGTTGGCCTGTGCCGCCCCTGTTCGTGGGGCTCATGGTGGTGTGTAACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2751.2;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                        Disclosure; Columns 75-78; 73pp; English.
                                                                                                                                                                                                                            cyclase, is activated by Gsalpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.7%;
Matches 3080; Conservative
(TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endocrine deficiencies
                                                                                              2000-578539/54
                                               3
                                                                                                                        P-PSDB; AAB02010.
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Page

999	720	780	840	900	960	1020	1080	1137	1197	1257	1317	1377	1437	1497	1557	1617 1669	1677 1729
CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGACTAACGTGGTGCTGGGATCCTGGCG	GCAGTGCAGGTCGGGGGCGTTTCGCAGCAGCCCGGCGGGCCCTCTGGGGGCCTCTGG	TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCATCCGCATGCGGGCTGCC	GTCCTCAGGGGCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACGT	GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAAC	GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG	ACCOGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGGGGGGG	CIGCIGCIGCIGGIATICCCCCAGCACGITGCCAIGGAGAIGAAGAAGACAICAACACA	AAAAAAGAAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC	CIGITIGCAGACATIGAGGGCTICACCAGCCTGGCATCCCAGTGCACTGGGCAGGAGCTG	GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTG	CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTCAGGGCTGCCGGAGGCCCGG	GCCGACCATGCCCACTGCTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	GTACGTGAGGTGACGGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG	CACTGCGGCGTCCTTGGCTTGCGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACC	CTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCACTCGCGGCAACA	CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAAGCGCAAGCGCAACGCG	TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCCA
601	661	721	781 830	841	901 950	961	1021	1081	1138	1198	1258	1318	1378	1438	1498 1550	1558 1610	1618
Qy Db	Qy	Qy	Qy Db	Qy	Qy	Oy Dp	o do	oy Ob	Oy Db	Qy Db	QY	Qy Dp	Qy Dp	Qy	QY Db	QY	Qy Db

CGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTCCAGAGAGGAGGATTTTGAGAAGAAG 1977 ATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC 2757 CGCCTAAACTTCCTCGGAAACTACAGGCAACAGGGGAAAAAGAGGGGAGATGGAGGAGCTA 2817 GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG GAGGATGAGGTGGATGCATCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCTGATGCTTGGGATT CATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTTGTGTTACTTCTGCCATTGCCAAC ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCCACCCAAGATGCCCTGAACCCT TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTACTCCTGT CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCC ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC Qy Dp Qy OY Db οy g g ò οý

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The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase, adenylate cyclase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian heart failure. The present CDNB sequence encodes human partial cardiac adenylcyclase VI (ACVI) isoform which is used for generating a third beta-ASP transgene, used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide encoding a modified adenylylcyclase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -
                                                          /*tag= a /product= "Human partial cardiac ACVI isoform #2" /note= "CDS does not include start and stop codon" /EC_number= "4.6.1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         636 TAACGTGGTGCTGGGCATCCTGGCGGCAGTGCAGGTCGGGGGGGCGCTTTCGCAGCAGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TAACGTGGTGCTGGGCATCCTGGCGCCAGTGCAGGTCGGGGGCGCTTTCGCAGCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             696 GCGCAGCCCCTCTGCGGGCCTCTGGTGCCCTGTGTTCTTTGTATACATCGCATACACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCTCAGCGCCAGGCCTTTCAGGAGCCCGCAGTTACATCCAGGCCCGGCTCCACCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 115-119; 153pp; English.
                    Location/Qualifiers
1..1812
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99.9%;
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Matches 1809; Conservative
                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-418260/44.
P-PSDB; AAE04309.
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                                                                                                                                                                 WO200148164-A2
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                                                                                                                                                                                                                                                                                      27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                      Hammond HK,
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                       Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3530 TICCTCAATGGGGGCCCCAGCAGTTAGCAGAGGGCACGAGTGGAAATTCAACCAAAGGGA 3589
                                                                                                                                                                                                                                                                                                       GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3057
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                                                                                 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG
                                                                                                                                                                                                                          ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG
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                                                                                                                                                                                                                                                                                                                                                                                     GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                            TTCCAGATGAAGATTGGGCTGAACATGGGCCCCAGTCGTGGCAGGTGTCATCGGGGCTCGG
                                                            CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCCAAGGACGTGGCGGCCCACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human partial cardiac adenylcyclase VI (ACVI) isoform #2
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1443 CTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACGGTGCT	2136 GATCTGTGCTGTGTACTCCTGTGGTTCTCTTAGGCCCTGCAAGGTCTGCCGCACGTCCCCGCGCAAGGTCTGCCGCGCGCG	2196 CAGCATTGTCGCTCACGGGACATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTGT	2256 GTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATAGGAACTGTGC	2316 AGCCCGGATGCTGAATTTAACACCTGCTGACAFCACTGCCTGCCACCGCAGCAGCACAAA	2376 TTACTCTGGGCC 	OY 2436 TGAGGTGTC 2445 	RESULT 9 AAV23246 ID AAV23246 standard; cDNA; 2127 BP.	AA AC AAV23246; XX XX 17-JUL-1998 (first entry)		KW transgene; gene therapy; congestive heart failure; cardiac function; KW adenovirus; ss. XX XX QS Homo sapiens.	Key CDS	;		WO9810085-A2. 12-MAR-1998.	PF 05-SEP-1997; 97WO-US15610. XX	XX PA (COLL-) COLLATERAL THERAPEUTICS. PA (REGC) UNIV CALIFORNIA. XX	PI Gao M, Hammond HK, Insel PA, Ping P, Post SR; XX DX WPI; 1998-193633/17. DR P-PSDB; AAW53345.	XX PT Vectors containing transgene(s) encoding beta-adrenergic signalling
GCATGAGAATCGGCAGCAGGAGCGGCTGCTGCTGGTATTGCCCCAGCACGTTGCCAT 1055	GGAGATGAAAGACATCAACACAAAAAAAGAGACATGTTCCACAAGATCTACATACA	GAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATC 1175 	CCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAA 1235 	SCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGT 1295 	GTCAGGGCTGCCGGAGGCCCGGGCCGACGATGCCCACTGCTGTGGGAGATGGGGGTAGA 1355 	CATGATTGAGGCCATCTCGCTGGTACGTGACAGGTGTGAATGTGAACATGCGCGT 1415 	GGGCATCCACAGCGGGCGCGTCCACGCGCGTCCTTGGCTTGCGAAATGGCAGTTCGA 1475 	GTGTGGTCCAATGATGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCG 1535 	CATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGG 1595 	CCGTGGTGGCAAGGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCT 1655 	GGGCGCCAGCCAGAAACGGAAAGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCG 1715 	GGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGAC 1775 	CAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGG 1835 	CACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGGATCCTGAGCCGTGCCATCGA 1895	GCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTCCA 1955 	GAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGT 2015 	PAATTTCCCACA 	CTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCT 2135

congestive heart of gene therapy Fig 12A; 114pp; English for useful present 60; proteins Claim The

from the present invention. The present invention describes a recombinant replication-defective viral particle (I) comprising a gene encoding a beta-adrenergic signalling protein (beta-ASP) operably linked to a promoter. Also described are: (1) a recombinant pro-viral plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably linked to a promoter and further comprising a replication-defective viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3) an isolated polynucleotide comprising a sequence encoding a human adenylicyclase isoform VI (AC-VI), or a variant having AC activity; (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide comprising the polynucleotide of (3); (1) can be used to form a comprising the polynucleotide of (3). (1) can be used to form a cardiac function in mammals. sequence encodes human adenylylcyclase isoform VI

T; 2 other; Sequence 2127 BP; 421 A; 637 C; 615 G; 452

ö 1115 1175 1235 1295 GCATGAGAATCGGCAGCAGCAGCGGCTGCTGCTGTCGGTATTGCCCCCAGCACGTTGCCAT 1055 GTCAGGGCTGCCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGTGGAGATGGGGGGTAGA 1355 815 995 677 695 755 875 935 617 797 917 977 437 497 557 857 377 Gaps GCGCAGCCCTCTGCGGGCCTCTGGTGCCCTGTGTTTGTATACATCGCATACACGCT GATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAA GTCTCAGCGCCAGGCCTTTCAGGAGCCCGCAGTTACATCCAGGCCCGGCTCCACCTGCA GCATGAGAATCGGCAGCAGCGGCTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCAT GAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATC CCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAA GCGCAGCCCCTCTGCGGGCCTCTGGTGCTCTTTGTATACATCGCATACACGCT CCTCCCCATCCGCATGCGGGCTGCCTCCTCAGCGGCCTGGGGCCTCTCCACCTTGCATTT 2127; ó DB 19; Length Score 1808.4; I Pred. No. 0; 0; Mismatches 51.0%; Conservative Best Local Similarity Matches 1809; Conserv Query Match 1056 318 378 558 8/9 1116 969 438 816 498 918 738 1176 989 936 966 1236 756 798 828 918 1296 978 ò g ò g ò g ò g οy g ò g à g ò q ò g ò g δ g

1655 1397 1457 2015 2075 2195 2117 1157 1895 1697 1877 1997 2057 1757 CATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGG GGGCGCCAGCCAGAAACGGAAAGAGGAGAAAAGGCATGCTGGCCAAGCTGCAGCGGACTCG GGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGAC CATGATTGAGGCCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 1038 CATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAAATGTGAACATGCGCGT TGTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCG CCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCT CAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGG TGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTCCA GAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGT TGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACA CTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCT GATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCG GTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGC GTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGC TTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCC 1476 1536 1218 1716 1776 1458 1518 1896 1638 2016 2076 2136 1878 1938 2316 2058 1356 1416 1098 1158 1596 1278 1656 1338 1398 1836 1578 1956 1698 1758 1818 2196 2256 2376 g a οy gg δý g δy g Óγ g δy g ŏ qq δy g οý g οy qq δ g οy g δ g δy g ò g Ω g ò g Ω

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 922 GCGCGGCCCCCGCTCCAGCTGCCCTACCTGGCCGTGCTGGCGGCCGCCGTCGCGCGTGATC 981
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                                               CCCAGGAGTGGGCGATCCTGCTGGCGCCGTTTGGTGCAGTGTTCCAGTCGAAGCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes the human type V adenylyl cyclase (hAC5) of the invention. hAC5 has a similar putative structure to other adenylyl cyclase isoforms but, like type VI, is distinguishable in that it has a larger N-terminus and a relatively shorter C-terminus as it lacks the C2b region. The hAC5 polypeptides are useful in assays that screen for potential therapeutic agents, which modulate hAC5 activity. These polypeptides are also useful in assays for the diagnosis of diseases and disorders. Agonists of hAC5 are useful control agents in such assays, and they may have useful effects in vivo for treating disease. Antibodies acting as (ant)agonists have diagnostic and therapeutic effects, and are useful in immunoassays for hAC5. (Antiagonists are particularly useful in treating diseases caused by abnormal hAC5 activity (e.g. In the heart and brain), and in diseases which are alleviated by modulating hAC5 activity. The oligonucleotides are useful in methods that inhibit or regulate hAC5 expression in vivo and in vitro. The cloning of the human isotype of AC5 enables the development of tissue-specific and selective pharmacological agents for use in treating particular human diseases associated with hAC5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGAGGGGCGGCCCAGGCAAGGGCAAGGAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 GAGGATACCGAGGTGACAACGACAGCGGGGGGGGACGGCTGAGGTGGCGCCCCGACGCGGTG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newly isolated and purified human type V adenylyl cyclase (hAC5) polypeptide - useful for identifying potential therapeutic agents that modulate hAC5 activity, and for the diagnosis of hAC5-associated diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4523;
                                                                                                                                                                                                                                      cyclase; human; hAC5; heart disease; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4523 BP; 840 A; 1419 C; 1428 G; 836 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.0%; Score 1703.4; DB 20; 71.3%; Pred. No. 0;
                                                                                                                                                                                                      Human type V adenylyl cyclase coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig la-h; 40pp; English.
                                                                                                        AAX00462 standard; DNA; 4523 BP.
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97US-0070901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORT-) COR THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                              98WO-US13540.
                                                                                                                                                                        (first entry)
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              2118 TGAGGTGTTC 2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-106048/09.
P-PSDB; AAW30600.
                                                                                                                                                                                                                                                     therapy; diagnosis;
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TGAGGTGTCC
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01-JUL-1997;
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Matches 2356;
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2436
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à a	1411	CGCGTGGGCATCCACAGCGGGCGCGCGCGCGTCGCGCGTTGCGAAATGGCAG 1470 L	
2	1471	153	
· 8	1882	94	
oy GB	1531	GGCCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAG 1590 	
οy	1591		
q	2002	CCAGGCTGTGGGGCGCGAGCGCTACCTCAAGGGCGCACAGTATCGAGACCTTCCTC 2061	
ογ Op	1651	ATCCTGGGCGCCAGCCAGAAACGGAAAGGGAAAAGGCATGCTGGCCAAGCTGCAGCGG 1710 	
δ	1711		
g	2122	18	
ò	1771	81	
2	7977	AACCACCIGGGTGGCAACCAGGIGICCCAAGGAGGATGGATGGGCTTTGAAGACCCC 2241	
Š a	1819	AGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGTTC 1878	
δy	1879	CTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGG 1938	
Op	2296	CIGGGCCGTGCCATTGACGCCAGGAGCATTGATAGGCTTCGGTCTGAGCACGCCGCAAG 2355	
Oy Dp	1939 2356	TITITGCICACCITCCAGAGAGATITIGAGAAGAAGTACTCCCGGAAGGTGGATCCC 1998 	
Qy	1999	CGCTTCGGAGCCTACGTTGCCTGTGGCCCTGTTGTGCTTCATCTGCTTCATCCAG 2058	
٥y	2059	211	
a B	2476	ATCACCATCGTGCCCCACTCCATATTCATGCTCAGCTTCTACCTGACCTGTTCCCTGCTG 2535	
Oy Dp	2119 2536	CTGCTAATCACCGTGCTGATCTGTGCTGTGTCCTGTGGTTCTGTTCCCTAAGGCC 2178 	
Oy Dp	2179	CTGCAACGTCTGTCCGGAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATC 2238	
δ	. 5	229	
අු	2656		
δý	2299	CCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACCTGCTGGTGACATCACTGCCTGC	
QQ	2716	GACCTGCTGGGCTTGGCACAGGAGCACACATCAGCGCGAGCCAGGTCAGGGTGT 2775	
op g	2359	CACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGC 2412 	
δλ.	2413	247	
ΩΩ	2836	CCCTGGCCCAACTGCAACTTCCCCGAGTACTTCACCTACAGCGTGCTGCTCAGCCTGCTG 2895	

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Left ventricular tissue of canine heart was used as a source of mRNA. A cDNA library was prepd. in lambda gt10 phage. A 970 bp Aat-HincII fragment from type I adenylyl cyclase cDNA was used as probe. The clones isolated were used to obtain cDNA encoding CACV. This probe may also be used to screen a human cardiac cDNA library to obtain the cDNA encoding human CACV. CACV, its analogues and antibodies are useful in therapy or diagnostic assays, e.g. in modifying and determining cardiac function. A decrease in CACV content of the heart contributes to impaired cAMP prodn. and in heart failure. The CACV can also be used to screen for cpds. which stimulate or inhibit
                                                                                                                                                                                                                                   type
                                                                                                                                                                                                                              solated nucleic acid mol. encoding Cardiac adenylyl cyclase - useful for determining and modifying cardiac function
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462 645 402 522 705 765 642 825 702 885 Gaps CACCCTGCGGGCCCCCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGG CCCAGGCAAGGGCAAGGAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGA CGGCGGCCTGCTGCCGCGCGCGCTGCAGATCTTCCGCTCCAAGAAGTTCCCGTCGGAC ATGGTGGTGTGTAACCGGCATAGCTTCCGCCAGGACTCCATGTGGGGTGAGTAACGTG CTCGGTGGAGCTGGGCCTGGACGAGCGGGGGGGGGGGGCCGCGGGGCCCGAGCCCGA GGGCGATCCTGCTGCCGCCGTTTGGTGCTGCTTCCAGTCGAAGCAGTTCCGTTCGGCC AAGCTGGAGCGCCTGTACCAGCGGTACTTTTCCAGATGAACCAGAGCAGCCTGACGCTG CTGGTGGCGGTGCTGCTGCTCACAGCGGTGCTGCTGGCTTTCCAAGCCGCACCCGCC CGCCCTCAGCCTATGTGGCACTGTTGGCCTGTGCCGCCGCCCTGTTCGTGGGGCTC GTGCTGGGCATCCTGGCGGCAGTGCAGGTCGGGGGCGCCTTTCGCCAGCAGCCCGCGCAGC GGTGACAACGACGGGGGGGGGCGCTGAGGTGGCGCCCGACGCGG--TGCCCCAGGAGT CTCATGGCCGTGCTGGTGCTCGTGTGCTGGTGCTGGCCTTCCACGCGGCGCGCCCC Query Match 47.6%; Score 1688.4; DB 14; Length 4356; Best Local Similarity 70.1%; Pred. No. 0; Matches 2347; Conservative 0; Mismatches 981; Indels 20: 346 225 285 343 165 406 466 526 403 586 463 646 523 902 991 ò 셤 qq qq g δ q o d ò οy à g QΥ δλ 셤 δ 셤

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cyclic AMP; adenosine monophosphate; screening; stimulation;
inhibition; treatment; cholera; pituitary tumour; heart failure;
ischaemia; endocrine disorder; cell necrosis;
pseudohypoparathyroidism; endocrine deficiency; human; ss.
                                                                                                                                                                                                                                                                                                                                               3643 GTCAAGGGCAAAGGCGAGATGATGATGATTTCCTCAACGGTGGGCCC 3690
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/product= Type V adenylyl cyclase
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A recombinant Adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzymes and the allows easier screening of compounds that stimulate and inhibit Adenylyl cyclase activity. The recombinant adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimera of adenylyl cyclase condition and a chimera of adenylyl cyclase condition and a chimera of adenylyl cyclase continued for screening inhibitors and stimulators of adenylyl cyclase activity. Inhibitors of the enzyme are useful for treating cholera, pituitary tumors, heart failure, ischaemia, endocrine disorders and cell necrosis. Stimulators of adenylyl cyclase are useful for treating pseudohypoparathyroidism and other
                                                                                                                                                    Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl cyclase, is activated by Gsalpha
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(TEXA ) UNIV TEXAS SYSTEM
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345 GCGATCCTGCTGCCGCTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAA 404 128 GGGCGCTGCCTGCCTTGCTGCAATATTCCGCTCTAAGAAGTTCCCGTCGGACAA 187 464 247 524 307 584 367 644 427 704 487 764 547 824 607 Gaps CTCTGCGGGCCTCTGGTGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCAT 188 ACTGGAGCGTCTGTACCAGCGCTATTTCTTCCGCCTGAACCAGAGCAGCCTCACCATGCT CCCTCAGCCTGCCTATGTGGCACTGTTGGCCTGTGCCGCCCCTGTTCGTGGGGGCTCAT GGTGGTGTGTAACCGGCATAGCTTCCGCCAGGACTCCATGTGGGGTGGTGAGTAACGTGGT 368 TGGCTCTGCAACCGTGCAGCCTTCCACGACCACAGGGCCTGGCCTGCTATGCGCT GCTGGGCATCCTGGCGGCAGTGCAGGTCGGGGGCGCTTTCGCAGCAGCCCGCGCGCAGCCC CATTGCAGTGGTGGTCGTCCAGGTAGTGGGCCTGTTGCTGCCACACAGCGCGC CCGCATGCGGGCTGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGC 405 GCTGGAGCGCCTGTACCAGCGGTACTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCT Length 3924; Score 1648.2; DB 21; Lengt Pred. No. 0; 0; Mismatches 873; Indels 46.4%; ilarity 71.4%; Conservative Best Local Similarity Matches 2265; Conservat Match 465 248 525 308 585 645 428 705 488 ò g ö g ò QQ ŏ g QΥ g οχ Dp ò g q

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Human; adenylyl and guanylyl cyclase; ADGUC-2; cardiovascular disorder; anapina peetoris; mycoardial infarction; vision disorder; keratitis; iritis; cataract; neurological disorder; epilepsy; Alzheimer's disease; pick's disease; stroke; mental disorder; mood and anxiety disorder; reproductive disorder; infertility; endometriosis; impotence; asthma; smooth muscle disorder; migraine; bacterial infection; gene therapy; transgenic animal; vaccine; enzyme; ss.
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CAAGGCAGGCAAGACCCACATCAAGGCTCTTGCAGACTTCGCCATGAAGCTGATGGACCA
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P-PSDB; AAE17130.
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31-AUG-2000;
22-SEP-2000;
29-SEP-2000;
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Novel human adenylyl and guanylyl cyclases and polynucleotides encodi the cyclases, useful for treating, diagnosing or preventing cardiovascular, neurological, vision, reproduction and smooth muscle disorders

5; Page 112-113; 116pp; English Claim

The invention relates to human adenylyl and guanylyl cyclases (ADGUC) preferably ADGUC1-ADGUC5 and nucleic acid molecules encoding such preferably ADGUC1-ADGUC5 and nucleic acid molecules encoding such polypeptides. ADGUC sequences are useful in the diagnosis, prevention and treatment of cardiovascular disorders (e.g. angina pectoris, myocardial infarction, ischaemic heart disease, hypertension and atherosclerosis), vision disorders (e.g. extratoconjuctivitis sicca, keratitis, iritis, cataract), neurological disorders (e.g. epilepsy, Alzhelmer's disease, pick's disease, Huntington's disease, dementia, parkinson's disease, pick's disease, Huntington's disease, dementia, mental disorders including mood and anxiety and prion diseases including kuru), reproductive disorders (e.g. infertility, endometriosis, importence, uterine fibroid and gynaecomastia), smooth muscie disorders (e.g. arrhythmias, asthma and migraine) and bacterial infections.

ADGUC polynucleotides are useful for creating knock-in humanised animals or transgenic animals to model human diseases. They are useful in sommatic or generaline gene therapy. ADGUC polynucleotides are also useful cor detecting differences in the chromosomal location due to the individuals abcur or difference in the part and part or affected individuals abcur or difference in the part propertion of the part of the pa individuals. ADGUC polypeptides are useful in a number of drug screening techniques and in vaccines. The present sequence is human ADGUC-2 cDNA.

Sequence 3137 BP; 553 A; 973 C; 1044 G; 567 T; 0 other;

5 1008 CGGAGGGGCGCCCAGGCAAGGCCAAGGAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTC 273 Gaps CGGCGGGGCGAAGGGGCGCGCCGGCCGACGAGCTGGAGGCCGGCGCGCCGTCGAGGGCGGCGAG GAGGATACCGAGGTGACAACGACAGCGGGCGGGACGGCTGAGGTGGCGCCCGACGCGGTG GGTCCGGGGATGGCGGCAGCTCGGCGGCTCGGGCTCGGGCGCGGGGCCCGGCGCGGTG CCCAGGAGTGGGCGATCCTGCTGGCGCCGTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTC CGTTCGGCCAAGCTGGAGCGCCTGTACCAGCGGTACTTTTCCAGATGAACCAGAGCAGC CTGACGCTGCTGGTGCTGGTGCTGCTCACAGCGGTGCTGCTGGCTTTCCAAGCC GCACCCGCCCCCCCTCAGCCTATGTGGCCACTGTTGGCCTGTGCCGCCCCCTGTTC AGTAACGTGGTGCTGGCCATCCTGGCGGCAGTGCAGGTCGGGGGCGCTTTCGCAGCAGAC 93; 500; Indels Length Score 843; DB 24; Pred. No. 7.6e-195; 0; Mismatches GCGCGCCCCCGCTCCAGCTGCCCTACCTGGC-23.8%; 68.4%; Matches 1286; Conservative Similarity Query Match Local 214 712 274 772 889 949 1009 1041 334 832 514 1120 394 454 694 g g g δ Op Q Dp g q à Ω g Qγ οy óγ οy ÓΥ g

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CTCCTCCCCATCCGCATGCGGGCTGCCGTCCTCAGCGGCCTGGGGCCTCTCCACCTTGCAT

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1818 2313 1180 CTGCTGCCCGTGCGCATGCGGGCCGCAGTGCTCAGCGGGGGTGCTCCTGTCCGCCCTCCAC 1239 CAGCATGAGAATCGGCAGCAGCAGCGGCTGCTGCTGTCGGTATTGCCCCAGCACGTTGCC 1054 ATGGAGATGAAAGAAGACATCAACACAAAAAAAGAAGA---CATGTTCCACAAGATCTAC 1111 ATACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTG 1540 ATCCAGAAAACATGACAACGTGAGCATCCTGTTTGCTGACATCGAGGGCTTCACCAGCTG GCATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTT GACAAGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTAC TGTGTGTCAGGGCTGCCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGTGGATGGGG GTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATG CGCGTGGGCATCCACACAGGGGCGCGTGCACTGCGGCGTCCTTGGCTTGCGGAAATGGCAG 1840 CGTGTGGGAATTCACAGCGGCGAGTACACTGCGGTGTCCTTGGTCTCAGGAAGTGGCAG TTCGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCT CCAGGCCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTC ATCCTGGGCGCCAGCAGAAACGGAAAGAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGG 1711 ACTCGGGCCAACTCCATGGAAGGCCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCC CAGAGAACCAACTCCATCGGGCACAACCCACACACTGGGGGGGTGAGCGCCCTTCTAC -- CGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGCCATTGATGATTCC 2200 AACCACCTGGGTGGCAACCAGGTGTCCAAGGAGATGAAGGGGTTTGAAGACCCC AGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGAGTTC A-----AGGACAAGAACGCCCAGGAGAGTGCGAACCCTGAGGATGAAGTGGATGTTT 1240 crescearcecerececaceaecaaceceaesaacaarrecrecrecrasaacaaecrecrecrec AATGTGCTGCTGTTCCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAG GTGTCTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTACATCCAGGCCCGGCTCCACCTG 1531 GCCCGCATCCACATCACTCCGGCCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAG TTGATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCC 1600 1960 2080 2140 1819 1171 1231 1471 2020 2260 1900 1591 1651 934 994 οqα g g g ò g ά g ò QQ δ g δ q Ω qq ò g Qγ g οy g QY Qλ Óχ g ò g δ g δy Q ă q οy ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A recombinant Adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzyme which allows easier screening of compounds that stimulate and inhibit Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimner of adenylyl cyclase (2 domains linked covalently. The domains may be linked by a linker peptide. The recombinant adenylyl cyclase is useful for screening inhibitors and stimulators of adenylyl cyclase activity. Inhibitors of the enzyme are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl cyclase, is activated by Gsalpha
                                                                                                                CTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGGGAGGACCATGTGCGCCGG
                                                                     CTGGGCCGTGCCATTGACGCCAGGAGCATTGATAGGCTTCGGTCTGAGCACGTCCGCAAG
                                                     TITITGCTCACCTTCCAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCC
                                                                                                    CGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAG
                                                                                                                                                                                                                                                                                                                         Adenylyl cyclase; type I; type II; recombinant; enzyme; cAMP, cyclic AMP; adenosine monophosphate; screening; stimulation; inhibition; treatment; cholera; pituitary tumour; heart failure; ischaemia; endocrine disorder; cell necrosis; pseudohypoparathyroidism; endocrine deficiency; human; ss.
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                  endocrine disorders and cell necrosis. Stimulators of adenylyl cyclase are useful for treating pseudohypoparathyroidism and o
                                                                                                                                                                          Length 3978;
treating cholera, pituitary tumors, heart failure, ischaemia,
                                                                                                                       BP; 708 A; 1213 C; 1275 G; 782 T; 0 other;
                                                                                                                                                                       16.8%; Score 595; DB 21; 51.9%; Pred. No. 2.1e-134;
                                                                                                                                                                                                                            0; Mismatches 1485;
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                                                                     endocrine deficiencies
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                                                                                                                       Sequence 3978
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Matches 1750;
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Scoring table:

Searched:

Title: Perfect score:

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US-09-097-5
Sequence 5, Application US/09008097
Sequence 5, Application US/09008097
Setent No. 6306830
GENERAL INFORMATION:
APPLICANT: Hammond, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Ening', Pelpei
APPLICANT: Post, Steven R.
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: GENE FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
COTATY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,097
US-08-997-362-123
US-09-095-855-123
US-09-234-542-123
US-08-997-080-176
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US-09-097-855-173
US-09-08-855-173
US-09-205-426-173
US-08-486-273-444
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ATTORNEY/AGEN, INFORMATION:
NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22000-20567.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  FILING DATE:
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    CITY: F
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-07-793-961A-1
US-08-726-214-11
US-09-708-097-3
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length
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No. Result

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           Length
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           DB
           Score 3549;
Pred. No. 0;
; Mismatches
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; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
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Matches 3513; Conservative
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US-09-474-076-1
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LENGTH: 4942
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APPLICAMY: Tonlinson, James E.
APPLICAMY: COR Therapeutics, Inc.
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5028-01-0S
CURRENT PELLIKO DATE: 1999-12-12
PRIOR APPLICATION NUMBER: US/09/474,076
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/070,904
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 08/086,550
PRIOR APPLICATION NUMBER: 08/086,550
PRIOR PLING DATE: 1997-07-01
PRIOR PLING DATE: 1997-07-01
PRIOR PLING DATE: 1997-07-01
PRIOR PLING DATE: 1997-07-01
SOFTWARE: PALENTIN UNSE: 1907-07-01 GTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGCTAC 3420 CAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGGGGAGATGACCACCTACTTC 3480 CTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCACAAATTCAGCTGAAGGGACCAAG 3540 61 GAACGCAAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120 204 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180 324 Gaps 9 1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 3241 CAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGGAAG CCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACGGGG <u>ښ</u> Length Indels DB 4; 36; 98.0%; Score 3478.4; 98.9%; Pred. No. 0; ive 0; Mismatches TYPE: DNA ORGANISM: human type VI adenylyl cyclase

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4084	00	60 04	20 64	80 24	40 84	00	60	20 64	80	40	00	60 104	020 164	080 224	137 284	197 344	257 404	317
CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGCGGCCCAGGCAAGGCAAGGCAAGGCAAGGCCAAGCCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG	GAGCTGGGGCTGCGGGCGTGGCCCTGGGCTTCGAGGTACCGAGGTGACAACGACAGCG 3	GGCGGGACGCCTAAGGTGCCCCCACGCGGTGCCCAGGAGTGGGCGATCCTGCTGCTGCCCC 3	CGTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC 4	CAGCGGTACTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGTG	CTGCTCACAGCGGTGCTGCTGCCTTTCCAAGCCGCACCCGCCCG	GTGGCACTGTTGGCCTGTGCCGCCCCTGTTCGTGGGGCTCATGGTGGTGTGTAACCGG 6	CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTAACGTGGTGCTGGGCATCCTGGCG 6	GCAGIGCAGGICGGGGGCCTITCGCAGCAGACCCGCGCAGCCCCTCTGCGGGCCTCTGG 7	TGCCCTGTGTTTTTTGTATACATGGATACACGCTCCTCCCCATCCGCATGCGGGCTGCC 7	GTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT 8	GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGCTTCTCTGCACCAAC 9	GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 9	ACCCGCAGTTACATCCAGGCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1	CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGAGAGAAGAAGAACATCAACACA 1	AAAAAAGAGGAGCATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1 	CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTG 1	GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTG	CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGG 1
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oy ob	Qy Dp	Oy Dp	Qy Dp	Qy Op	dy Dp	Oy Dp	oy Dp	og G	oy G	oy Op	Qy Dp	ço G	Qy Dp	Oy Dp	oy Oy	Qy Dp	Oy Dp	δ

1557 2217 2397 1464 1377 1524 1437 1584 1497 1644 1704 1617 1764 1677 1824 1737 1797 1944 1857 2004 1917 2064 1977 2124 2037 2184 2097 2244 2157 2304 2364 2277 2424 2337 2484 CGGAAGGACCATGTGCGCCCGGTTTCTGCTCACCTTCCAGAGAGGAGGATCTTGAGAAGAAG CTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCG CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT TGCTTCATCTGCTTCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT CCTGCTGACATCACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCT GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG GAGGAGAAAGGCATGCTGGCCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGTGTACTCCTGT GGTTCTCTGTGTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA GCCGACCATGCCCACTGCTGTGGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 2245 1405 1318 1465 1525 1438 1585 1498 1645 1705 1618 1765 1825 1738 1885 1798 1945 2005 1918 2065 2125 2038 2185 2098 2305 2218 2365 2278 2338 1378 1558 1678 1858 1978 2158 2425 g οy a δŽ g Qy Db ōλ Q Qγ g ογ Q Qy Db 9 9 9 9 Ω Qγ qq Q Dp Qγ Ωp δy g οy g ٥y q Óγ q óγ g ò

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OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII from DW4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 19911118
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4046 base pair:
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                                         AAGGTGGGCACT 3549
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                 3625 TTCCTCAATGGGGGCCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3684
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90.9%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                            Character-
                                                                                                                                                                                                                                                   APPLICANT: YOSHINITO ISHIKAWA
TITLE OF INVENTION: Cloning and Character
TITLE OF INVENTION: ization of a Cardiac
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alan M. Gordon
ADDRESSEE: Alan M. Gordon
STREET: 1937 West Main Street,
STREET: P.O. Box 60
CITY: STAMFORD
STATE: Connecticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/07/793,961A
                                                                                                                                                                                                 Sequence 1, Application US/07793961A Patent No. 5334521 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: GOLDO, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/CDCKET NUMBER: 31,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203 321 2719
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC AT
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240 367 300 424 424 484 484 544	8 0 4 9 0 7 9	784 720 844 780 904 840	9000 1024 960 1084 11144 1080	H 8 5 7 6 9 H
CCTCGGTGCCCTGGCAGGATGACGCCTTCATCCGGAGGGCGGCCCAGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCCAGGAGAGGCCAGGAGAGGCCAGGAGAGGCCAGGAGAGGCCAGGGCAAGGCCAGGAGAGCCCCGGGCAAGGCCAGGAGAGCCCCGGGCAAGGCCAGGAGAGCCCGGGCAGGAGAGCCCGGGCAGGAGAGCCCGGGCAGGAGAGAGAGAGAGAGAGAACGAGGCGGC	36CGGTGCTGGT 36CGGTGCTGGT TCAGCCTGCCTA 11111111111111111111111111111111111	ACAGCTITCGCCAGGGACTCCATGGGTGGTGAACTACGTGGTGCTGGGCATCCTGG CAGTGCAGGTGGGGGGCCTTCGCAGCAGCCCCCCAGCGCCCTCTGCGGGCCTCT C	GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGCTCCTCTGCACCCAAC [AGATCTACATACAGAAGCATGACAATGTCAGCAT
181 308 241 368 301 425 485	421 545 605 605 665 601	4 6 8 7 4 8 0	965 901 1025 961 1085 1021	1081 1205 1138 1265 1198 1325 1258
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1444 1377 1437 1497 1557 1617 1741 1737 1797 1981 1977 2037 2097 2157 2281 2217 2341 2401 2337 2397 1504 1564 1624 1681 1921 1798 CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT 1857 2101 2161 2221 CATAGCACCGCAGTTGGCCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC 2277 2461 1445 GCAGACCATGCCCACTGGTGTGGAGATGGGGGTGGACATGATCGAGGCCATCTGGTG CTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCG 1738 ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC 2042 CGGAAGGACCATGTGCGCCCCTTCCTGCTCCACAGAGGAGGATCTTGAAAAGAAG GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG 1625 CTGGCCAACCATATGGAGGCGG---CCCGGGCCGGCCGATCATCACCCGGGCCACG 2102 TACTCAAGGAAGGTGGACCCCCGCTTCGGAGCCTACGTGGCCTGTGCGTCTTC CCTGCTGACATCACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCT GCCGACCATGCCCACTGCTGTGGAGATGGGGGTAGACATGATTGAGGCCCATCTCGCTG 1678 GAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT 1438 1565 1498 1922 1858 1982 2162 2342 1558 1918 1978 2038 2098 2158 2282 2218 2278 2402 2338 Qy Db 9 2 2 g ò ద 0.y Db QY δ ΩD Ω QC δ Q oy Db QΩ ò QΩ δ qq δ QQ οy qq οý D Q g οy q δ

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Score 2990.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                Cyanamid Company
Plaza
                                                                                                                                               Sequence 1, Application US/08240357
Patent No. 5578481
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,637
REGISTRATION NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 90.9%;
Matches 3229; Conservative
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MEDIUM TYPE: Floner
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US-08-240-357-1
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TITLE OF INVENTION: Cloning and Characterization of TITLE OF INVENTION: Cardiac Adenylyl Cyclase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: MEDIDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,357
FILING DATE: 10-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: DB 1;

us-09-750-240-5.rni

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3 & 5	483	GICTGGCCCCAGGTCGAGGCGCTCCGCCCGCTCGGCCAAGCTGGAGCGCCCTGTA AGCGGTACTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGT ACCGCTAACTTTTCCAGATGAACCAGAACCAGAACACAACAACAACAACAACAACAACA
O.Y Db	8 0	TGCTCACAGGGGGCGCGCTTTCCAAGCCGCCCCCCCCCC
Oy Dp	541 665	CCTGTGCCGCCGCCCTGTTCGTGGGGCTCATGGTGGTGTGTAAACGG 60
oy Op	601 725	CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTAACGTGGTGCTGGGCATCCTGGCG 660
Qy Db	661 785	GCAGTGCAGGTCGGGGCGCTTTCGCAGCAGCCCGGCAGCCCCTCTGCGGGCCTCTGG 720
9 0 0	721	TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCATCCGCATGCGGGCTGCC 780
O.Y DD	781 905	GTCCTCAGCGGCCTGCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT 840
Oy Db	841 965	GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAAC 900
Oy Db	901	GTCATTAGCATCTGCACCACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 960
O.y D.b	961 1085	ACCCGCAGTTACATCCAGGCCCGGCTCCACTGCAGCATGAGAATCGGCAGGAGCGG 1020
O. O.	1021	CTGCTGCTGCTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080
Oy Dp	1081	AAAAAAGAAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1137
Qy Dp	1138	CTGTTIGCAGACATIGAGGGCTICACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTG 1197
Qy Dp	1198	GTCATGACCCTGAAFGAGCTCTTTGCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC 1257
Oy Dp	1258 1385	CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTCAGGGCTGCCGGAGGCCCGG 1317

1497 1857 2097 2277 2461 2457 1437 1624 1557 1677 1737 1861 1797 1921 1917 2041 1977 2037 2157 2217 2341 2401 2337 2397 1377 1564 1801 1981 2101 2161 2221 2281 2521 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG CTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA GAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA CATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC ATGTTCACCTGTAACCACACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA 1682 1802 1862 1798 1858 1982 1918 1978 2102 2038 2162 2222 2402 1318 1445 1378 1505 1438 1565 1498 1625 1558 1678 1738 1922 2042 2098 2158 2282 2218 2342 2278 2338 2462 2398 q qq δ QQ δy g δý q δý В ŏ qq δy Q Db ò qq δ QQ qq Q g q qq g qq ò g Qγ δ ŏ δ Qγ á οy ò

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                                                                                                                                                                                    APPLICANT: Tang, Wei-Jen
APPLICANT: Tang, Wei-Jen
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
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MEDIUM TYPE: Floppy disk

COMPUTER: Eloppy disk

COMPUTER: El PO COMPATIBLE

COMPUTER: TEM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN BAPA:

APPLICATION NUMBER: US/08/726,214

FILING DATE: CONCURTENTLY HERWITH

CLASSIFICATION: 435

PRIOR APPLICATION WHERE: US 60/005,498

FILING DATE: 04-OCT-1995

ATORNEY/AGRNT INFORMATION:
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                          CITY: Houston
STATE: Texas
COUNTRY: United States of America
2IP: 77210
                                                                                                                                                                                                                                                                                  Durkee
                                                                                                                                      Sequence 11, Application US/08726214
Patent NO. 6107076
REBAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMAL.
ITLE OF INVENTION: AND USES THEREI
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTURNITY ACELL THE CALLED IN NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD.
TELECOMMUNICATION INFORMATION:
TELEPAN: (512) 474-757
INFORMATION FOR SEO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: Arnold, White &
STREET: P.O. Box 4433
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293	GAGCTGGGGCTGCGGTCAGTGGCCTTGGGTTTTGATGACACTGAGGTGACCACACCG 349
301	. GGCGGGACGGCTGAGGTGGCCCGAGGAGTGGGCCGATCCTGCTGCGCGC 360
361	CGTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC 420
421	. CAGGGGTACTTTTTCCAGATGAACCAGAGCTGACGCTGCTGGTGGCGGTGGTGGTG 480
481	CTGCTCACAGGGGTGCTGCTGGCTTTCCAAGCCGCACCCGCCCTCCAGCCTGCCT
541 590	GTGGCACTGTTGGCCTGTGCCGCCCTGTTCGTGGGGCTCATGGTGTGTGT
601	CATAGCTTCCGCCAGGACTCCATGTGGGTGAGTAACGTGGTGCTGGGCATCCTGGCG 600
661 710	GCAGTGCAGGTCGGGGGCGCTTTCGCAGCAGCCGGCAGCCCCTCTGGGGGCCTCTGG 720
721	TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCCCCATCCGCATGCGGGCTGCC 780
781	GECTCAGGGGCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACGT 840
841	GGTGATGCCTTCTCGGAAGCAGCTCGGTGCCAATGTGCTGTTTCCTCTGCACCAAC 900
901	1 GTCATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGGCCCAGCCCTTTCAGGAG 960
961 1010	ACCCGCAGTTACATCCAGGCCCGGCTCCACTGCAGGAGTCGGCAGCAGGGGGGGG
1021	. CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAGACATCAACACA 1080
1081	- AAAAAAGAAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1137
1138	CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTG 1197
1198 1250	B GTCATGACCCTGAATGAGCTCTTTGCCGGTTTGACAAGCTGGCGGGGAATCACTGC 1257
1258	CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTCAGGGCTGCCGGAGGCCCGG 1317
1318	GCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 137

GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCCATCCACAGCGGGCGCGTG TACCTCAAGGAGCAGCACTTGAGACTTTCCTCATCCTGGGCGCCCAGGAAACGGAAAA GAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC CAGATGGGCATTGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTACTCCTGT GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA AIGITCACCIGTAACCACACCCCCATACGGAGCIGTGCAGCCCGGAIGCIGAATITAACA CCCCTGTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC CCTGCTGACATCACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCT ŏ g Óλ q QΥ g OY Db Qy Dp QZ DD οy Db Qy g Sy qq ΟŸ qq Q D oy Oy g á qq δ qq ò g δy g ò Db

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APPLICANT: Hammond, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Dird, Peipei
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/008,097 FILING DATE:
                                                                US-09-008-097-3; Sequence 3, Application US/09008097; Patent No. 6306830; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFRAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: Coding Sequence; LOCATION: 1...1812; OTHER INFORMATION: US-09-008-097-3
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99.9%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
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Best Local Similarity 99.9
Matches 1809; Conservative
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PRIOR APPLICATION DATA:
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CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2517
                                                                                                                                                                            CTGCTGAGTCTCTTGGCCAGCTCCTCCTCCACATCAGCAGCATTGGCAAGCTAGTT
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	274 GAGGATACCGAGGTGACAACGACAGCGGCGGGACGGCTGAGGTGGCGCCCGACGCGTG 333	CCCAGGAGTGGGCGCCCCTTTGGTTGGGTTCCAGGTGCAGGGTTCCAGGTTCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCAGGTTCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCAGGTTCCAGGTTCAGGTTCCAGGTTCAGGTTCAGGTTCCAGGTTC	745 Crereceredecerecerecerecerecereces and references and refer	394 CGTTCGGCCAAGCTGGAGCGCCTGTACCAGCGGTACTTTTCCAGATGAACCAGAGCAGC 453		crcaccardcrcardcccgrdcrcgrcgrccrcdcrcardrrargradgccrrcacdcg	514 GCACCCGCCCCCCCCGCCCTGCCTGTTGGCCTGTTGGCCTGTGCCGCC	GTGGGGCTCATGGTGTGTGAACCGGCATAGCTTCCGCCAGGACTCCATGTGGGTGG	982 CICATCATGGCTGGGCTTGGCTGGCGCGCCTTCCACCAGGACCACATGGGCCTGGCC 1041 634 AGTAACGTGGTGGGCATCCTGGCGGCAGTGCAGGTCGGGGCGCTTTTCGCAGTAGAC 693		694 CCGCGCGCAGCCCTCTGCGGGCCTCTGTGTTTTTTTTTT		754 CICCICCCATCGCAIGCGGGCTGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCAT 813	TTGATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCC		AATGTGCTGCTGCTCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGG	AATETTUTUATTTTUTUUGGAUGAUAAUATUGTIGGTIGTUTGCAUCCAUTATUUGGGUTGAG	934 GIGICICAGGCCCAGGCCTITCAGGACACCGCAGITACAICCAGGCCCGGCTCCACCTG 993 11 1 1 1 1 1 1 1 1 1	CAGCATGAGAATCGGCAGGAGGGGCTGCTGTGGTATTGCCCCAAGAAGTGGTTGCC				1111 ATACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTG 117		1171 GCATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTT 123		1 GACAAGCTGCCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTAC 129		TGTGTGTCAGGGCTGCCGGGCCGGCCGACCATGCCCACTGCTGTGGAGATGGG 13
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1530 1590 1770 1998 2415 2118 1650 2295 2715 ------CGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCC 1818 AGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTC 1878 CTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGG 1938 CIGCIAAICACCGIGCIGAICIGIGCIGIGIACICCIGIGGIICCICIGIICCCIAAGGCC 2178 CTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGCACATAGCACCGCAGTTGGCATC 2238 TTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACC 2298 ATCCTGGGCGCCAGCCAGAAACGGAAAGAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGG 1710 rgcgtctcggggctgcctgaagcaagggctgaccacgcccactgctgtggagatgggc 1761 CAGAGAACCAACTCCATCGGGCACAACCCACACACGGGGGGCTGAGGGCCCCTTCTAC GTAGACATGATGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATG GGCCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAG ACTCGGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCC CTGGGCCGTGCCATTGACGCCAGGGGCATTGATAGGCTTCGGTCTGAGCACGTCCGCAAG CTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTG CGCGTGGGCATCCACAGCGGGCGCGTGCACTGCGGGCGTCCTTGGCGTAATGGCAG TTCGATGTGTGTCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCT CCAGGCCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTC TTTTTGCTCACCTTCCAGAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCC CGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAG CACCTGCAGCAG-----CTCAATTACTCTGGGCCTGGATGCTCCCCTGTGAGGGC

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Sequence 9, Application US/08726214
Patent No. 6107076
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 448-3000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        COUNTRY: United States of ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3924 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 71.4
Matches 2265; Conservative
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
                                                                                                                                                                                                                   Houston
3493 CCC 3495
                      3910 CCC 3912
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        ACCATGCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTG
                                                       GCCAGCTCTGTCTTCCTGCACATCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTG
                                                                                                       GGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTGACAACTAT
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                                                                                                                                                     GACCTACTGCTTGGCGTCCATGGCTTGTTCTTCCAATGAGACCTTTGATGGGCTGGAC
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                                                                         CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
                                                                         ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.4%; Score 1648.2; 71.4%; Pred. No. 0;
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GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gliman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADI
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
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Qy Db	705	CICTGCGGGCCTCTGGTGCCTGTGTTTTGTATACATGCCATACACGCTCCTCCCCAT 764
Qy	765	CCGCATGCGGGCTGCCGTCCTCAGCGGCCTGCTGCCATTGCATTTGATCTTGGC 824
Qy	825	CTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCT 884
Qy Db	885	GTTCCTCTGCACCAACGTCATAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCG 944
Qy Db	945	CCAGGCCTTTCAGGAGACCCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAA 1004
Qy Db	1005	TCGGCAGCAGGAGCGGCTGCTGTCGCTATTGCCCCAGCACGTTGCCATGGAGATGAA 1064
Qy Db	1065 848	agaagacatcaacacaaaaaagaagaCatgttccacaagatctacatacagaagca 1121
Q.y D.b	1122	TGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTG 1181
Q _V	1182 968	CACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGC 1241
Qy Dp	1242	TGCGGAGAATCACTGCCTGAGGATCAGATCTTGGGGGACTGTTACTACTGTGTGTG
QY Dp	1302	GCTGCCGGAGCCCGGCCGACCATGCCCACTGCTGTGGAGATGGGGGTAGACATGAT 1361
Qy Db	1362	TGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAACATGCGCGTGGGCAT 1421
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Qy	1482	GTCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCA 1541
Qy Db	1542	CATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGG 1601
Qy Db	1602 1388	TGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACTGAGACTTTCCTCATCCTGGGCGC 1661
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2009 2069 2189 2249 2041 2309 2369 2483 2543 2515 2101 2341 2603 2398 2663 2455 GGCAACAGGGGAAAAAGGGGGAGTGGAGGAGCTACAAGGCATACAACCGGAGGCTGCTGCTG 2843 CCCACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTAATCAC 2129 G-----CTCAATTACTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCAC 2423 2221 2281 GTATCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCCTCTGGAAACTACA 2783 2102 TIGCCIGGCAGAGGAGCACAACAICACGGIGAACCAGGIGAACGCAIGICAIGIGATGGA 2161 CTACGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCTGCTTCATCCAGCTTCTAATTTT GTCCCGCAGCATTGTCCGCTCACGGCACATAGCACCGCAGTTGGCATCTTTCCGTCCT TITGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTGACAACTATGACCTACTGCT ---CGIGCICATCGIAGAGGIGCCCGGIGICACACTCTITGACAACGCTGACCTICTGGT 2399 CACCGCCAATGCCATAG---ACTTCAGCAACAACGGGACCTCCCAGTGCCCTGAGCATGC -CGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAA CCGGGGCCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGC CATCGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGGTTTTTGCTCAC 2130 CGTGCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTCT GCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGGAG CTGCAGCTTTCCTGAGGTGTCCCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGT CTTCCTGCACATCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGGCTCATCTA CTTCCAGAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGC AGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTGGTGTTTGCGCTGGCGCCT TGGCGTCCATGGCTTGTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCTGC 1742 2010 2070 2162 2222 2484 1508 1622 1890 1682 1950 1802 1922 2190 2370 2424 2544 2342 2604 2664 2456 2724 2784 QQ g 8 Qy Db g ò g δ Q 셤 ŏ g ď g Qγ g δ g g g g q ò ά õ δ δ δ οŽ ò ò δ ò ŏ

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                                                                                                                                                                                                                                                                                                                              Length 3978;
                                                                                                                                                                                                                                                                                                                            Score 595; DB 3; I
Pred. No. 9.3e-138;
0; Mismatches 1485;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION: INFORMATION:
                                                                                                                     INFORMATION:
TELEFAX: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3978 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-726-214-1
                                                                                                                                                                                                                                                                                                                            Local Similarity 51.9%;
Matches 1750; Conservative
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 2576 GGCCACAGAAGAAGGAGGAGATGGAGGAGCTGCAGGCCTACAACCGGCGCTTGCTGCA 2635
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                                     2844 TAACATICIGCCCAAGGACGIGGCGGCCCACTICCIGGCCCGGGAGCGCCCCAAIGAIGA
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APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arrold, White & Durkee
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CITY: Houston
STATE: Texas
COUNTRY: United States of America
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US-08-726-214-1
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ACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAGACCCGCAGTTACATC	CAGGCCCGGCTCCACTGCAGCATGAGAATCGGCAGCAGGAGCGGCTGCTGTCGTA	TIGCCCCAGCACGTIGCCATGGACATGAAAGAAGACATCAACAAAAAAAAGAAGAAGAGATG	TTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAG 	GGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCTGAATGAG	CTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTG	GGGGACTGTTACTACTGTGTGTCAGGCTGCCGGAGCCCGGGCCGACCATGCCACTGC	TGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACGGT	GTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGCACTGCGGCGTCCTTGGC	TTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGACCTGGCCAACCACATGGAA	GCAGGAAGCCGGGCTGGCCGCATCCACTCGGGCAACACTGCAGTACCTGAACGGG	GACTACGAAGTGGAGCCGGGCGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCCCTCAAGGAGCAGCACACACA	5 ATTGAGACTITCCTCATCCTGGGCGCCCAGCAGAAACGGAAAGGGAAAGGCATGCTG	5 GCCAAGCTGCAGCGGACACACACATGGAAGGGTGATGCCGGATGGGTTCCT	5 GAICGIGCCITCICCGGACCAAGGCITCCAAGGCCTICCGCCAGAIGGGCAITGAIGAI 	TCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCTGAGGATGAGGTGGATGAG	S TTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGC	CGGTTTTGCTCACCTTCCAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGG CGGTTTTGCTCACCCTTCCAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGG
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2415 2406 3015 2295 2175 2475 2595 2655 2436 2775 2556 2895 2676 2955 2736 CCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATC 2055 GCCCGCCAGATGG---AGCTGGAGATGGCAGACCTGAACTTCTCACCCTGAAGTACAAG 1948 GTTCTGGCTCTCATTCTGCCCCTTGTTCTGCCTTCTAATAATCCCACAG AGTGTGGCTGTCCTGCTGCTGTGTTCTGCATCTGCTTCCTGGTGGCCTGTGTCTG GCGCCCCATGCCTGCTGTGCGGCCTCGTGCCTCCCCCTGCCGCCATATTCCTGCGG GCGGCCCAGGCAGGAGGAGGGGATGACATGGAGAAGTGAAGTGAAGCTGGACAACAAGAGG CAAGCTGAGCGAGAGGAAAGTACCACCAGCTTCAGGACGAGTATTTCACCAGCGCCGTG ATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCAC CTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTGACAACTATGAC CTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGT ----GGTACACGAAGGCCATG GGGGCCGGTGCCATCTCAGGGCGCAGCTTCGAGCCGATCATGGCCATCCTGCTATTCTCG CTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCCTGTGG AACTICICIGAGIICIAIGIGGAGCIGGAGGCAAACAAIGAGGGIGCCGAGIGCCIGCGG CTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAG CTTCTGAATGAGATCATCGCTGACTTTGATGAGCTCATGGACAAAGACTTTTACAAGGAC CAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTG CTGCTGCTAATCACCGTGCTGATCTGTGTGTACTCCTGTGGTTCTCTGTTCCCTAAG GCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGC TACCTACACATCACCCGGGT------CCAGTGTTTTCCAGGGTGCCTGACCATCC ACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCC 2356 TGCCACCTGCAGCAGCTCAATTACTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACC 2416 ATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTGGCC 2228 recrearcirarerresegeseccesearcerecrecie-recesecereces AGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTTGGGG 2656 CCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTGGTGTTTGCG AAACTACAGGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTACAGGCATACAACCGGAGG CTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCCACTTCCTGGCCCGGGAGCGCCGC AATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTTATGTTTGCCTCCATTGCC CTGGAGCTCAGCG------2008 2536 2236 3016 1996 1888 2296 2476 2596 2407 2437 2557 2956 1831 2056 2116 2176 2068 2117 2176 2347 2836 2896 2677 a οy g OY Db OY Db 90 AQ ολ g Q Dp 0 y 0 y DP QY g δy Dp Qy Dp Q Dp οy g QΥ g οy g Q

3076 CTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCCTCAGGGCTGAACGCC--- 3132

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GGAGACCCGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGA 1016
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                                                     3247 AAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGGAAGCCACAG
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                                      ----AGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCTGACTACGCC
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Pred. No. 1.6e-115;
0; Mismatches 1488;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09412210
Patent No. 6403358
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYC.
FILE REFERENCE: 5800-47
CURRENT APPLICATION NUMBER: US/09/412,210
CURRENT FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 3518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 21529 adenylate cyclase
NAME/KEY: CDS
LOCATION: (247)...(3480)
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ilarity 50.0%;
Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
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COUNTRY: Unit
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       FILING DATE: CONCURTENTLY HERWITH CLASSIFICATION NUMBER: US/05/249 PRIOR APPLICATION DATE: CONCURTENTLY HERWITH CAPLON DATE: APPLICATION NUMBER: US 60/005,498 FILING DATE: 04-OCT-1995 ATTORNEY/AGENT INFORMATION: NAME: Highlander, Steven I. REGISTRATION NUMBER: 37,642 REFERENCE/DOCKET NUMBER: UTSD:450 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION HOS SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 4601 base pairs TYPE: nucleic acid STRANDEDNESS: single
APPLICATION NUMBER: US/08/726,214
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Matches 1439; Conserv
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ESULT 12 5-08-307-896-5 Sequence 5, Application US/08307896C Patent No. 6034071 GENERAL INFORMATION:

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                                                                                                                                                                                        Length 4008;
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
FILLE REPERBUCE: 29770
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILLING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                        Query Match 12.9%;
Best Local Similarity 50.8%;
Matches 1370; Conservative
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; ORGANISM: Rattus norvegicus
US-08-307-896-5
                                                                                                                        LENGTH: 4008
                                                                                                          SEQ ID NO 5
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US-08-726-214-3
Sequence 3, Application US/08726214
Fatent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
Thexas
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COMPUTER: IBM PC compatible
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COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                           Score 459; DB 3; I
Pred. No. 4.9e-104;
                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 1240;
                                                       FILING DATE: CONGULTERILLY HETEWITH CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Stewen L.
REGISTRATION NUMBER: 37,642
REFERNENCE/OCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 418-3000
TELEFAX: (512) 44-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                            APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                         12.9%;
50.8%;
              SOFTWARE: Patentin Rela
                                                                                                                                                                                                                                                                                                                                                                                                          Matches 1370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                            US-08-726-214-3
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3189 GCGGCTCATGGAGCAGATGAGCACATGAGCACTCCTTCAACAATTTCCAGATGAA 3248
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                                                                                                                                                               2727 TCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCCTCTGGAAACTACAGGC 2786
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 2343 TGAGTTAAAAATGTTAATCATGATGGTGGCACTCGTGGGCTACAACACCATTCTACTCCA 2402
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                                 2607 CGTCCAIGGCTIGGCTTCTTCCAAIGAGACCTTIGAIGGGCTGGACTGTCCAGCTGCAGG
                                                                                                 2667 GAGGGTGCCCCTCAAATATATGACCCCTGTGATTCTGCTGGTGTTTGCGCTGGCGCTGTA
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RESULT 14

PCT-US95-11808-5

Sequence 5, Application PC/TUS9511808

GENERAL INVENTATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS

CORRESPONDENCE ADDRESS:
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1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4008;
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                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/11808 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.9%; Score 459; DB 5; I 50.8%; Pred. No. 4.9e-104; Ive 0; Mismatches 1240;
                                                                                                                                                                                                                                                                                  PRICE APPLICATION DATA:

APPLICATION NUMBER: US 08/307,896
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S.
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29970 165/28755
TELEPHONE: (212) 408-2500
TELEPAX: (212) 765-2519
TELEPAX: (212) 765-2519
TELEFAX: 650 6111063
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
and
Donohue
                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Brumbaugh, Graves,
                                30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4008 base pairs
TYPE: nucleic acid
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                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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Matches 1370; Conserv
                                                                                                      10112-0228
                                                                      New York
                                                 New York
                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                     COUNTRY:
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                                                                      STATE:
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	2 TGAGGCCATCTCGCTGGTACGTGAGGTGACGGTGTGAAATGTGAACATGCGCGTGGGCAT	2 CCACAGCGGGGGGGGGGGGGGGGGGGGGAATGGCAGTTGGATGTGTG 	2 GTCCAATGATGACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGTGGCCGCATCCA	2 CATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGG	2 TGGCAAGGCGCAACGCGTACCTCAAGGAGCAGCACTTGAGACTTTCCTCATCCTGGGCGC	2 CAGCCAGAAACGGAAAAGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAA	2 CTCCATGGAAGGGCTGATGCCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGA	2 CTCCAAGGCCTTCCGCCAGATGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCA	2 AGATGCCCTGAACCCTGAGGTGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCG	2 CAGCATIGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTTGCTCACCTTCCAGAGAGA	2 GGATTITIGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTG	2 IGCCCTGITGGTCITCACTICATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCAC	2 CCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGAT	9 CIGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACG	7 TCTGTCCGGGAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGT	7 CCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACCCCCATACG	7 GAGCTGTGCAGCCCGGATGCTGATTTAACACCTGCTGACATCACTGCCTGC	7 GCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCTGTGAGGGCACCATGCCCACCTG
1104	1362	1422	1482	1542	1602 1404	1662	1722	1782	1842	1902	1962	2022	2082	2139	2187 1983	2247	2307	2367
qq	Qy	Qy Db	Qy	oy Og	Qy Db	QY Db	QY Dp	Oy Db	Oy Dp	Qy Dp	Qy Dp	Q _Y	oy Dp	QX Dp	Oy Db	Qy Dp	Oy Dp	οy

2639 2486 2342 2666 2459 2726 2519 2786 2846 2699 2966 2759 3026 2819 3086 2879 3146 2939 2999 TTTCCTGAGCAACTCTGAGGAGACAACCCTTCCCACTGCCAATACATGCAAATGCAAACGT 2222 GCGGCTCATGGAGCAGATGAAGCACATGAAGCACTCCTTCAACAATTTCCAGATGAA 3248 3368 CCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGA 3428 3485 2343 TGAGTTAAAAATGTTAATCATGATGGTGGCACTCGTGGGCTACAACACCATTCTACTCCA CGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCTGCAGG CACCCATGCC---CATGTTCTGGATGCGTACAGCCAGGTCCTGTTTCAGAGACCAGGCAT 2460 TIGGAAAGACCTGAAGGCTCCGTGTCACTCCCATATTCTTCATCACGCTGCT 2727 TCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCCTCTGGAAACTACAGGC CAAAAAAGGGGGGGGGGGGGGGTAGAAACCATGGAGAACCTAAAATCGAGTGCTGCTGGAGAA CATTCTGCCCAAGGACGTGGCGGCCACTTCCTGGCCCGGGAGCGCCGCAATGATGATGAACT GATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAAGAT TGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACGGGGGTCCCCGA CAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTGGCCCAGCTCTGTCTT TTCTGTCCCGGATAACCAGGCGTCGATTCTTCATGCTCGAAACTTGTTTTCCTCCCGTA CCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTTGGGGCTCATCTATT GGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTGACAACTATGACCTACTGG GAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTGGTGTTTGCGCTGGCGCTGTA AACAGGGGAAAAAGAGGAGGAGGAGGAGCTACAGGCATACAACCGGAGGCTGCTGCATAA 2640 CGTGCTTCCTGCACACGTGGCTGAACACTTCCTGGCCAGGAGCCTGAAAAATGAGGAGCT GTTCTATGTGGAGCTGGAGGCAAACAATGAGGGTGCCGAGTGCCTGCGGGCTGCTCAACGA GATCATTGCTGACTTTGATGATCTGCTTTCTAAGCCAAAGTTCAGTGGTGTTGAAAAGAT GTGTCGAGGGGTGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTACTTCCTCAA 2163 2547 2667 2520 2787 3147 3180 2427 2223 2487 2283 2607 2403 2580 2847 2967 3027 2820 3087 2880 3189 3120 3369 3429 δλ g δý Q O. Db δ g oy ob g y g δ g δ QQ δ d οŽ Dp δ ga A Dp ŏ g qq g 셤 셤 ò ò δý ò

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                                 Sequence 5, Application US/08726214

Patent No. 6107076

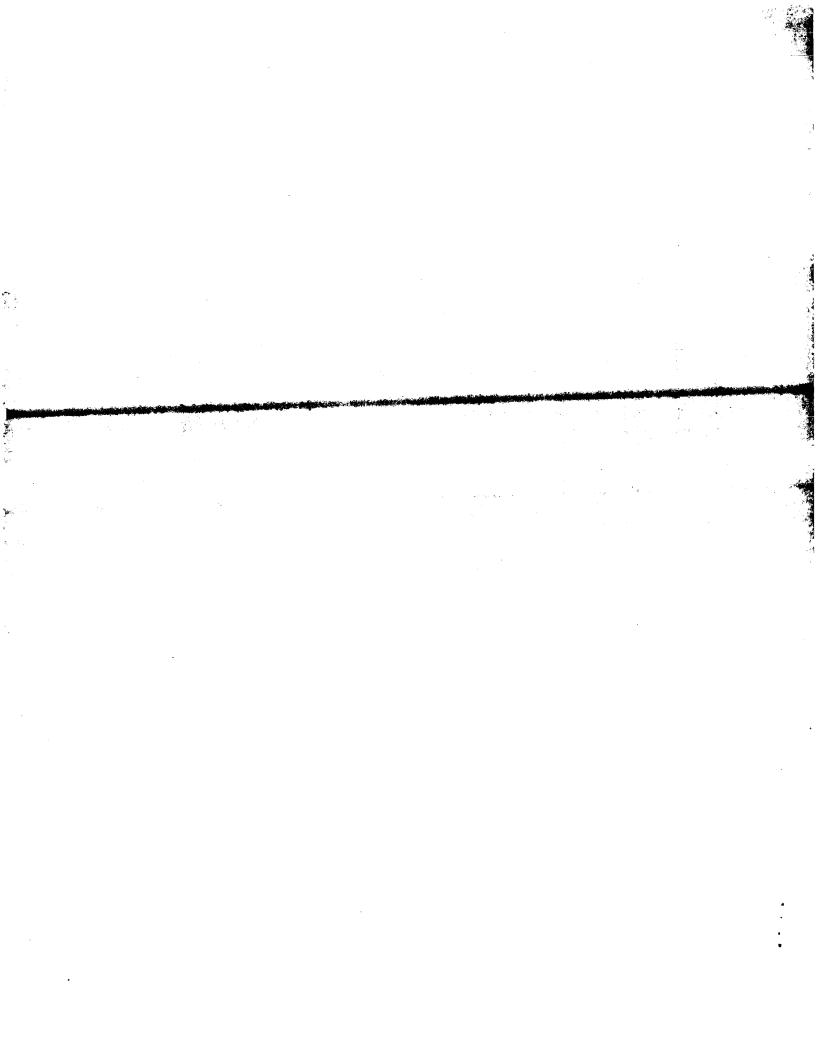
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENILYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
STREET: P.O. Box 4433
COUNTY: Houston
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.4%; Score 441.6; DB 3; Best Local Similarity 50.1%; Pred. No. 1.1e-99; Matches 1359; Conservative 0; Mismatches 1284;
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REPERSNEKD/COKET NUMBER: UTSD:450
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-7577
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4533 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                        -08-726-214-5
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1560 AGGATCAAGATCTTGGGGGACTGTTACTACTGTGTCAGGGCTGCCGGAGGCCCGGGCC 1320 1630 GGTGGCGTCCTGGGCCCAGAAGCGCTGGCAGTATGATGTTATGGTCTACCGATGTCACTGTG 1689 1561 CAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCGTAC 1620 GAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATG 1740 1869 GACAGCTCAAAATGGCCTCAACGGCTCGGCCCTGCCAAACGGAGCACCGGCATCCAAGCC 1928 1741 CCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAGGACTCCAAGGCCTTCCGCCAG 1800 1929 CAGCTCCCCTGCCCTTATTGAGACCAAGGAGCCCAATGGGAGTGCCCATGCCAGCGGCTC 1988 1801 ATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAG 1860 2049 CCGCCGCAGGCTGCGCCTCCAGGACCTGGCAGACCGTGTGGGACGCCTCTGAGGATGA 2108 2040 CTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCTGATGCTTGGGATTTA 2099 2100 TGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGTGG 2159 2349 crircergerregagagarrerecrerrearcergaccarerrerregargerecearerr 2408 GACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCCATCTCGCTGGTA CGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGCAC 1441 TGCGGCGTCCTTGGCTTGCGGAATGGCAGTTCGATGTGTGGTCCAATGATGTGACCCTG GCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACACTG 1861 GATGAGGTGGATGAGT-TCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCG 1980 CTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTCTG 2229 CTACTCGGTGGAGAAGGAAGCAGAGTGGGGGCTGCCTTCAGCTGTTCCTGTGTGGTCCT 2160 TTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCACA 2220 TAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACAT 2109 GCACGAACTGAACCAGCTTCTTAACGAGCCCTGCTGGAGCGGGAGTCCGCCCAGGTGGT 2169 AAAGAAGAAACACATTCCTCCTAACGATGAGGTTCATGGACCCAGAGATGGAAACACG

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2280 GTTCACCTGTAACCACACCCCCATACGGAGC-----TGTGCAGCCCGGATGCTGA
                              2469 GGCCAGAAATACCTGGGCCATGTTAGCCATCTTCATTCTGGTTATGGCCAATGTTGTGGA
                                                          2330 ATTTAACACCTGCTGACATCACTGCCTGCACCTGCAGCTCAATTACTCTCTGGGCC
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3548 ATGACATCIGGGGGAACACGTCAATGIGGCCAGCAGGATGGAATCCACAGGGGTCATGG 3607
                                                                                                                   ACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGG
                                                                       3608 GCAATATCCAGGTGGTAGAAGAGACACAGGTCATCCTTCGAGAGTATGGCTTCCGCTTTG
                                                                                                   3428 AGTGTCGAGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTACTTCCTCAATG
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Search completed: March 1, 2003, 04:06:06 Job time: 136.927 secs



Sequence 848, App Sequence 180, App Sequence 66, App1 Sequence 17, App1 Sequence 445, App Sequence 1351, App Sequence 1353, App Sequence 1353, App Sequence 1599, App Sequence 1599, App Sequence 123, App Sequence 173, App Sequence 176, App Sequence 176, App Sequence 176, App Sequence 176, App Sequence 177, App Sequence 178, App Sequence 177, App Sequence 178, App Sequence 177, App

Sequence 1 Sequence 4 Sequence 4 Sequence 4

Sequence Sequence

Perfect score: Sequence: Scoring table:

Searched:

Database

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DB 10; Length 3549;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09750240

Settlicant: Insel, P. A. APPLICANT: Insel, P. A. APPLICANT: Poing, P. APPLICANT: Osci, S. R. APPLICANT: Gao, M. TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART TITLE OF INVENTION: CONGESTIVE HEART TITLE OF INVENTION: CONGESTIVE HEART TITLE OF INVENTION: APPLICANT NUMBER: US 09/472,667

PRIOR APPLICATION NUMBER: US 09/008,097

PRIOR FILING DATE: 1999-12-7

PRIOR FILING DATE: 1997-09-05

PRIOR FILING DATE: 1997-09-05

PRIOR PELING DATE: 1997-09-05

PRIOR PELING DATE: 1997-09-05

PRIOR PELING DATE: 1996-09-05

NUMBER OF SEQ ID NOS: 13

SECTION OF SECTION NUMBER: US 08/708,661
US-09-933-797-165
US-09-964-531-848
US-09-764-868-180
US-09-989-442-66
US-09-764-868-182
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                                                                                                         US-09-764-868-1351
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                                                                                   US-09-764-869-445
US-09-728-445-487
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US-10-007-747-43
US-10-038-937-43
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100.0%; Pred. No. 0;
ive 0; Mismatches
 958

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; ORGANISM: Homo sapiens
US-09-750-240-5
 RESULT 1
US-09-750-240-5
Query Match
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Sequence 17, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 13, Appli
Sequence 181, Appli
Sequence 69, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 11, Appli
Sequence 17, Appli
Sequence 56, Appli
Sequence 792, Appli
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Sequence 791, Appli
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                                                                                             (without alignments)
15188.998 Million cell updates/sec
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                                                                                                                              US-09-750-240-5
3549
1 atgtcatggtttagtggcct.....aagggaccaaggtgggcact 3549
                                                                                 March 1, 2003, 02:24:48; Search time 145.712 Seconds
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                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpna/USO7_pUBCOMB.seg:*
/cgn2_6/ptodata/2/pubpna/DSO7_pUBCOMB.seg:*
/cgn2_6/ptodata/2/pubpna/USO6_bUBCOMB.seg:*
/cgn2_6/ptodata/2/pubpna/USO6_pUBCOMB.seg:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seg:*
/cgn2_6/ptodata/2/pubpna/DSO7_NEW_PUB.seg:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seg:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seg:*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
           GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                     460893 segs, 311809382 residues
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                                                                                                                                                                                                                                                                                                                                                          Published_Applications_NA:
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Listing first 45 summaries
                                                          nucleic search, using sw model
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Gaps

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Best Local Similarity 100, Matches 3549; Conservative

Score

Result Š. 61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120

1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60

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TTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTGGTC GACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTA TGCGGCGTCCTTGGCGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACCCTG 1561 CAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCGAACGCGTAC CTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCCCAGCAGAACGGAAAGAG 1681 GAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATG ATGGGCATTGATGATTCCAGCAAAGACAACCGGGGGCACCCAAGATGCCCTGAACCCTGAG 2041 TTCATCTGCTTCATCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATTAT 2221 AGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAATG CGTGAGGTGACAGGTGTGAATGTGAACATGCGGCGTGGGCATCCACAGCGGGCGCGTGCAC CAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCGTAC GATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGG TTCAFCTGCTTCAFCCAGCTTCTAATFTTCCCACACTCCACCCTGATGCTTGGGATTTAT TCTCTGTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCGTCACGGGCACAT AGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATG <u> AGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTGTCAGGGCTGCCGGAGGCCCGGGGCC</u> GCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGTGGT g ò g Qy Db 94 95 97 DP QY 07 QQ Dp QY Db Qy Db QQ οy ద q δ à

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CGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGCTAC 3420
                                                           GTCGAGGGGTGAGGTGAAGGCCAAGGGGGAGATGACCACCTACTTC 3480
                                                                                               GCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACCAAG 3540
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TION: FALLURE
1: 22000205525
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2001-10-12
1DATE: 2001-10-12
1TON NUMBER: US 09/472,667
ATTE: 1999-12-27
1TON NUMBER: US 09/008,097
ATTE: 1999-10-16
1TON NUMBER: US 08/924,757
ATTE: 1997-09-05
ATTE: 1997-09-05
ATTE: 1997-06-16
ATTE: 1997-06-16
ATTE: US 08/708,661
ATTE: US 08/708,661
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99.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                     Sequence 1. Application US/10201000
| Publication No. US20020187540A1
| GENERAL INFORMATION:
| APPLICANT: Tomilinson, James E.
| APPLICANT: Tomilinson, James E.
| TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF F. TITLE OF INVENTION: CYCLASE
| FILE REFERENCE: 44481-5028-01-05
| CURRENT APPLICATION UNDER: US/10/201,000
| CURRENT APPLICATION NUMBER: US/99/474,076
| PRIOR APPLICATION NUMBER: PCT/US98/13694
| PRIOR FILING DATE: 1999-12-12
| PRIOR FILING DATE: 1999-07-01
| PRIOR FILING DATE: 1999-07-01
| PRIOR PILING DATE: 1997-07-01
| PRIOR PILING DATE: 1997-07-01
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| NUMBER OF SEQ ID NOS: 2
| SOFFWARE: PATENTIN VET. 2.0
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Best Local Similarity 98.9%;
Matches 3513; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (145)..(3648)
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541 GTGGCACTGTTGGCCTGTGCCGCCCTGTTCGTGGGGCTCATGGTGTGTGT	601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTAACGTGGTGCTGGGCATCCTGGCG 	661 GCAGTGCAGGTCGGGGGCGCTTTCGCAGCAGCCCGCGCAGCCCCTCTGCGGGCCTCTGG	721 IGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCATCCGCATGCGGGCTGCC	781 GTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT [841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAAC	901 GTCATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGAG 	961 ACCGGCAGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 	1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA	1081 AAAAAAGAAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC	1138 CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTG	1198 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTG	1258 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGG	1318 GCCGACCATGCCCACTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTGGCTG	1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGGGGGCGCGTG	1438 CACTGCGGCGTCCTTGGCTTGCGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACC	1498 CTGGCCAACCACGTGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA	1558 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCG
Qy Dp	Oy Op	Qý Dp	Qy Db	O.y Db	Qy Db	oy B	Oy Dp	oy D	oy B	oy og	Oy Dp	Oy Dp	Oy Dp	Oy Dp	Oy Dp	Qy Db	Qy Db

oy.		TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCCA
g n	٥	ACCICAAGGAGCAGCATIGAGACITICCICAICCIGGGCGCCAGCCAGAAAAAAAA 182
QY	~	7
qq	1825	SAGAAGGCCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG 188
Qy	731	ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAGGACTCCAAGGCCTTCCGC 1797
qq	1885	CCGCGCTGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC 194
Οy	1798	S
qq	1945	AGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCT 200
Qy	1858	CCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG 1
qa	2002	SATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG 206
Qy	1918	TCCAGAGAGGATTTTGAGAAGAAG 197
QQ	2065	GGAAGGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGGATCTTGAGAAGAAG 212
Οy	1978	0
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Qy	2038	60
qq	2185	GOTICATCIGOTICATCAGCITCTCATCITCCCACACACCCTGATGCTTGGGATC 224
δλ	2098	TATGCCAGCATCTTCCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT 2157
qa	2245	ATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT 230
Qy	150	21
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qq	2365	Accacccantraccarciticarccractraratractracarraccarraccaac 24
QY	27	AIGITCACCIGIBACCACACCCCAFACGGAGCIGIGCAGCCGGGAIGCIGAATITAACA 2337
qq	2425	STICACCIGIAACCACACCCCCATACGGAGCIGIGCAGCCCGGAIGCIGAAITIAACA 24
Qy	2338	CCTGCTGACATCACTGCCTGCCACCAGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCT 2397
qq	2485	crecreacarcacreccaccrecaecrecaecreaarracrerereeecreeareer 25
δλ	2398	4
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Qy	2458	3AGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 25
ФД	2605	SCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCACATCGGGAAGTTGGCC 26
Qy	2518	<u>`</u>
qq	2665	TGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCACC 272
Qy	2578	ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2637
QQ	2725	TCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 278
Qy	33	TTTGATGGGCTGGACTGTCCAGGGGGGGGGGCCCCTCAAATATATGACCCCTGTG 2697
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                                           CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC
                                                  GGTGCCGAGTGCCTGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC
                                                                                                                            GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC
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APPLICANT: Hammon, H. K.
APPLICANT: Insel, P. A.
APPLICANT: Ping, P.
APPLICANT: Gao, M.
TITLE OF INVENTION: GNE THERAPY FOR CONGESTIVE HEART
FILLE REFERENCE: 220002056723
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09750240 Patent No. US20020103147A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     DB 10;
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                                                                                                                                                                                                                                                                    ; Score 3379.2;
; Pred. No. 0;
0; Mismatches
CURRENT FILLNG DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1996-09-05
NUMBER: OF SEQ ID NOS: 13
SOFTWARE: FASLERQ for Windows Version 4.0
SEQ ID NO S: 12
                                                                                                                                                        4.0
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US-09-750-240-12
                                                                                                                                                                                                                                                                    Query Match 95.2%;
Best Local Similarity 97.4%;
Matches 3458; Conservative (
                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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	TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCCATCCGCATGCGGGCTGCC	TGCCCTGTGTTTTTGTCTACATCGCCTACACGCTCCTCCCCATCCGCATGCGGGCTGCC GTCCTCAGCGGCCTGGGGCTCTCCACCTTGCATTGATCTTGGCCTGGCAACTTAACCGT [GGTGATGCCTTCCTCTGGAAGCAGCTGGTGCCAATGTTGGTGCTGGCCAGGCAACTTAACCGTGGTGATGCTGCTTCCTCTGCAACGCGTGCCAATGTGCTGCTGCTGCTGCTGCTGCACGAACGA	GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGGGCCAGGCCTTTCAGGAG	ACCCGCAGTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGCGGGGGGGG	CTGCTGCTGTCGGTATTGCCCCGGCACGTTGCCATGGAGATGAAGAAGACATCACACACA	AAAAAAGAAGACAIGTICCACAAGAICTACATACAGAAGCAIGACAATGICAGCATC	CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCAGCAGCTG	GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTG	CTGAGGATCAAGATCTTGGGGAACTGTTACTACTGTGTGTCTCAGGGCTGCCGGAGGCCCGG	GCGGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG 	CACTGCGGCGTCCTTGGCGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACCTCTCTCT	CTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCACATCACTCGGGCAACA	CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCGAACGCGGCAACGCAACGCGAACGCGAACGCAACGCAACGCAACAA	TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGGGCCCAGCAGAACGGAAA 167 	GAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG 173 	ATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCCTTCTCCCGGACCAAGGACTCCAAGGCTTCCTCGCAAGGACTCTAAGGCATTCCGC	

YIGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG AGGACCATGTGCGCCGGTTTTTGCTCACCTTCCAGAGAGGAGTTTTGAGAAGAAG CCCGGAAGGTGGATCCCGGTTCGGAGCCTACGTTGCCTGTGCCTGTTGGTCTTC GCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC TCACCTGTAACCACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA ATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG HIGAGGIGGAIGAGIICCIGAGCCGIGCCAICGAIGCCCGCAGCAIIGAICAGCIG CCCGGGAGCGCCCCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGGCGTGTT 1TGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT :TGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC ICTITGICITGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCC TTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGTTCTTCCAATGAGACC TGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC

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APPLICANT: Dest, S. R.,
APPLICANT: Bost, S. R.,
APPLICANT: GAO, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
FILE REFERENCE: 220002056733
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1999-10-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
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                                Version 4.0
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Windows
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Matches 1809; Conservative
SOFTWARE: FASTSEQ for W. SEQ ID NO 3
LENGTH
                                                                         TYPE: DNA ORGANISM: Homo sapiens
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US-09-750-240-3
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Publication No. US20030008371A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, James
APPLICANT: Cor Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION TITLE OF INVENTION: CYCLASE
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FILE REFERENCE: 44481-5027-01-US
CURRENT APPLICATION NUMBER: US/10/175,158
CURRENT FILING DATE: 2002-06-20
FRIOR APPLICATION NUMBER: US/09/473,716
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-07-01
PRIOR PLICATION NUMBER: 60/070,901
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.0
SECOLID NO 12
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US-10-175-158-1
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Qy Db	1054	ATGGAGATGAAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTAC 1110
Qy Dp	1111	ATACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTG 1170
Oy Dp	1171	GCATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTT 1230
Qy Db	1231	GACAAGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTAC 1290
Qy Dp	1291 1702	TGTGTGTCAGGGCTGCCGGAGGCCCGGCCGACCATGCCCACTGCTGTGGAGATGGGG 1350
Oy Db	1351 1762	GTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATG 1410
Oy Dp	1411	CGCGTGGGCATCCACAGCGGGGCGCTGCACTGCGCTCCTTGGCTTGCGAAATGGCAG 1470
Qy Dp	1471	TICGATGIGGICCAAGGIGGICCACCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCT 1530
yo da	1531	GGCCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAG 1590
oy Ob	1591	CCAGGCCGTGGTGGCAAGGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTC 1650
Qy Db	1651 2062	ATCCTGGGCGCCAGCCAGAAACGGAAAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGG 1710
Q _Y	1711	ACTCGGGCCAACTCCATGGAAGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCC 1770
O.y D.b	1771 2182	
O.y	1819	AGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTC 1878
oy Ob	1879	CTGAGCCGTGCCATGCCCGCAGCATTGATCAGCTGCGGAAGACCATGTGCGCCGG 1938
Qy Dp	1939 2356	TTTTTGCTCACCTTCCAGAGGAGGATTTTGAGAAGAAGTACTCCGGAAGGTGGATCCC 1998

2238 2358 2892 3309 2952 3012 3429 3072 2178 2715 2775 2412 2835 2472 2895 2532 2955 2592 3012 3069 2712 2772 3189 2832 3249 3369 2475 2655 2298 2652 3489 2058 3073 CAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCCTCAGGGCTGAACGCC 3132 ATCACCATGGGCCCACTCCATATTCATGCTCAGCTTCTACCTGACCTGTTCCTGCTG 2716 GACCTGCTGGCTGCTTGGCACAGGAGCACAACATCAGCGCGAGCCAGGTCAACGCGTGT CGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAG CTTCTAATTTTCCCACACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTG CTGCTAATCACCGTGCTGATCTGTGCTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCC CTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATC TTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACC ACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTG GCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTG GGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTGACAACTAT GACCTACTGCTTGGCGTCCATGGCTTGGCTTCCTTCCAATGAGACCTTTGATGGGCTGGAC TGTCCAGCTGCAGGGAGGGTGGCCCTCCAAATATATGACCCCTGTGATTCTGCTGGTGTTT CCTGAGCATGCAACCAAGGTGGCATTGAAGGTGGTGACGCCCCATCATCATCTCAGTCTTT TGGAAACTACAGGCAACAGGGGAAAAAGAGAGAGATGGAGGAGCTACAGGCATACAACCGG 2833 AGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCCACTTCCTGGCCCGGGAGCGC CGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCGTGTTATGTTTGCCTCCATT GCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAGGGTGCCGAGTGCCTG CGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGG CACCTGCAGCAG-----CTCAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGC 2473 1999 2416 2059 2476 2119 2536 2179 2596 2239 2656 2299 2359 2776 2413 2896 2533 2593 2653 3070 2713 3130 2773 3190 3250 2893 3310 2953 3370 3013 OY Db QQ Oy Oy g οqα Ωy Db Db Q Oy Dp OD Qy Db QQ δ 9 O.Y Db δ Oy Db δ δ ò δ ò οy g δ D οŽ g ò 60/235,834

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R APPLICATION NUMBER: 60/236, 369

R FILING DATE: 2000-09-19

R R FILING DATE: 2000-09-18

R APPLICATION NUMBER: 60/224, 519

R FILING DATE: 2000-07-26

R FILING DATE: 2000-07-26

R R FILING DATE: 2000-10-20

R R APPLICATION NUMBER: 60/249, 299

R PILING DATE: 2000-10-29

R APPLICATION NUMBER: 60/249, 299

R PILING DATE: 2000-10-29

R APPLICATION NUMBER: 60/244, 617

R R APPLICATION NUMBER: 60/244, 617

R R PILING DATE: 2000-10-20

R R PILING DATE: 2000-12-08

R PILING DATE: 2000-12-08

R R PILING DATE: 2000-09-25

R R PILING DATE: 2000-09-21

R APPLICATION NUMBER: 60/229, 343

R R PILING DATE: 2000-09-01

R APPLICATION NUMBER: 60/229, 345

R R PILING DATE: 2000-09-01

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R APPLICATION NUMBER: 60/229, 345

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R APPLICATION NUMBER: 60/229, 343
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R FILING DATE: 2000-10-02
R FILING DATE: 2000-10-02
R PILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/236,370
R FILING DATE: 2000-09-29
R FILING DATE: 2000-09-29
R FILING DATE: 2000-09-28
R FILING DATE: 2000-10-02
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R APPLICATION NUMBER: 60/237,040
R FILING DATE: 2000-10-02
R FILING DATE: 2000-10-20
R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/239,935
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APPLICATION NUMBER: 60/228,924
FILING DATE: 2000-08-30
APPLICATION NUMBER: 60/224,518
FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/229,509
FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/236,367
FILING DATE: 2000-09-29
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APPLICATION UNDHER: 60/234,274
FILING DATE: 2000-09-21
APPLICATION NUMBER: 60/234,223
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FILING DATE: 2000-10-13
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  FILING DATE: 2000-12-08 APPLICATION NUMBER: 60/
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  3550 TCTACCTACGACAAGGTGGGCAAGACCCACATCAAGGCACTGGCCGACTTGCCATGAAG 3609
                                                                                                                                                                                                                             3193 CTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATT 3252
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PUZON
FILE REPETRANTE: DS/09/989,442
CURRENT PILING DATE: 2001-11-21
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PRIOR FILING DATE: 2000-01-31
PRIOR PELING DATE: 2000-01-31
PRIOR PELING DATE: 2000-02-04
PRIOR PELING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-12
PRIOR PLILING DATE: 2000-09-14
PRIOR PLILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PLILING DATE: 2000-07-26
PRIOR PLILING DATE: 2000-07-16
PRIOR PLILING DATE: 2000-07-17
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R APPLICATION NUMBER: 60/226,868
R FILING DATE: 2000-08-22
R APPLICATION NUMBER: 60/216,647
R FILING DATE: 2000-07-07
R APPLICATION NUMBER: 60/225,267
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FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/251,869
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FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/225,757
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. Sequence 23, Application US/09989442
. Publication No. US20030013649A1
. GENERAL INFORMATION:
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PRICK PELING DATE: 2000-11-09
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PRICK APPLICATION NUMBER: 60/246,532
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PRICK APPLICATION NUMBER: 60/240,210
PRICK APPLICATION NUMBER: 60/225,681
PRICK APPLICATION NUMBER: 60/225,759
PRICK APPLICATION NUMBER: 60/225,719
PRICK APPLICATION NUMBER: 60/225,213
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PRICK APPLICATION NUMBER: 60/225,214
PRICK APPLICATION NUMBER: 60/235,314
PRICK PLILNG DATE: 2000-09-14
PRICK PLILNG DATE: 2000-11-17
PRICK APPLICATION NUMBER: 60/249,218
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PRICK APPLICATION NUMBER: 60/249,214
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PRICK APPLICATION NUMBER: 60/249,214
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3031 2732 ATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCCTCTGGAAACTACAGGCAACAG 2791 2852 TGCCCAAGGACGTGGCGGCCCACTTCCTGGCCCGGGAGCGCCGCAATGATGAACTCTACT 2911 3032 TCGCTGACTTTGATGAGATTATCAGCGAGGGGGTTCCGGCAGCTGGAAAGATCAAGA 3091 3152 GCCGCTCCCACATCACTGCCCTGGCTGACTACGCCATGCGGCTCATGGAGCAGATGAAGC 3211 ACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCAG 3271 3272 TCGTGGCAGGTGTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGA 3331 3392 IGTACCAGGITCTAGCIGCCAAGGGCIACCAGCIGGAGTGICGAGGGGIGGICAAGGIGA 3451 421 GCAAGACCCACATCAAGGCACTGGCCGACTTTGCCATGAAGCTGATGGACCAGATGAAGT 480 2912 ATCAGTCGTGTGAGTGTGGCTGTTATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCT 2972 ATGTGGAGCTGGAGGCAAACAATGAGGGTGCCGAGTGCCTGCGGGCTGCTCAACGAGATCA ö Length 837; Indels 3452 AGGCCAAGGGGGAGATGACCACCTACTTCCTCAATGGGGGCCCC 3495 AGGGCAAAGGCGAGATGACCTACTTCCTCAATGGAGGGCCC / Match 16.5%; Score 586; DB 9; I Local Similarity 85.3%; Pred. No. 1.7e-135; les 652; Conservative 1; Mismatches 111; PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR PILING DATE: 2000-10-20
PRIOR PAPLICATION NUMBER: 60/241,826
PRIOR PELLING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR PELLING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
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611 TGTACCAGGTGCTGCCTGCCAACACGTACCAGCTGGAGTGCCGGGGCGTGGTCAAGGTCA 670
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                                                                                                                                                                                   3452 AGGGCAAGGGGGAGATGACCACCTACTTCCTCAATGGGGGCCCC 3495
                                                                                                                                                                                                              671 AGGGCAAAGGCGAGATGATGACCTACTTCCTCAATGGAGGCCC 714
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CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 06/179,065
PRIOR PELITAGE DATE: 2000-01-31
PRIOR PLILING DATE: 2000-01-31
PRIOR PLILING DATE: 2000-02-04
PRIOR PLILING DATE: 2000-06-28
PRIOR PLILING DATE: 2000-06-28
PRIOR PLILING DATE: 2000-06-14
PRIOR PLILING DATE: 2000-07-11
PRIOR PLILING DATE: 2000-07-11
PRIOR PLILING DATE: 2000-07-11
PRIOR PLILING DATE: 2000-07-14
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PRIOR PLILING DATE: 2000-09-14
PRIOR PLILING DATE: 2000-09-17
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-29
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                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 181
LENGTH: 915
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85.2%; Pred. No. 1.6e-121;
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) LOCATION: (883)

: OTHER INFORMATION: n equals a,t,g, or c

US-09-764-868-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
LOCATION: (815)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
LOCATION: (852)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
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OTHER INFORMATION: n equals a,t,g, or
                                                   Sequence 181, Application US/09764868
Patent No. US20020168711A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.23
Matches 600; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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2000-11-1	ER: 6	. K.	R: 6	Z000-11-0 VUMBER: 60	2000-08-1 NUMBER: 60	-6	, 2,	2 0	NUMBER: 60 2000-09-0	NUMBER: 60	وفر	, 0	2000-09-0 VUMBER: 60	9-6	6.	9-6	۰	2000-09-0	-60-	2000-10-0	3	. e	. ~	10.	NUMBER: 60 2000-10-0	ا ف	و د	3-10- 3R: 6	- E	0-10-	0-10-	NUMBER: 60 2000-11-0	MBER: 6	MBER: 6	MBER	0-11-	ER: 0-08	E C	ER: 6	2000-08-1 NUMBER: 60	000-08-	-80-0	NUMBER: 60 2000-09-2
NG DATE:	PPLICATION	PPLICATION	ATION	LLING DATE: PPLICATION	ILING DATE: PPLICATION	ILING DATE:	ILING DATE:	DATE	ATION DATE:	TION TARE	TION		DATE	DATE	DATE	VTION DATE:	TION	DATE: ATION	ILING DATE	ILING DATE:	PPLICATION	PPLICATION	NG DATE: ICATION	ILING DATE:	PPLICATION ILING DATE:	PPLICATION	PPLICATION	LING DATE: PLICATION	ILING DATE:	ILING DATE:	ILING DATE:	APPLICATION ! FILING DATE:	PPLICATION ILING DATE:	PPLICATION	ILING DATE: PPLICATION	DATE:	PPLICATION ILING DATE:	PPLICATION	PPLICATION	ING DATE: LICATION	ILING DATE:	ILING DATE:	APPLICATION PFILING DATE:
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PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/215,135
PRIOR PAPLICATION NUMBER: 60/249,218
PRIOR PLILING DATE: 2000-08-14
PRIOR PLILING DATE: 2000-11-17
PRIOR PLILING DATE: 2000-09-08
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-14
PRIOR PLILING DATE: 2000-09-14
PRIOR PLILING DATE: 2000-09-14
PRIOR PPLICATION NUMBER: 60/231, 401
PRIOR PPLICATION NUMBER: APPLICATION NUMBER: 60/230,438

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Length 915; Indels

14.9%; Score 529.6; DB 9; 85.2%; Pred. No. 1.6e-121; 11ve 2; Mismatches 101;

Query Match 14.9 Best Local Similarity 85.2 Matches 600; Conservative

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2792 GGGAAAAAGAGGAGATGGAGGAGCTACAGGCATACAACCGGAGGCTGCTGCATAACATTC 2851
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           12 GRAGWAAAAGAGGAGAAGAAGGAGCAGCA-GCCTACAACCGGCGGCTGCTGCACAACATCC
                                                                                                                          2972 ATGTGGAGCTGGAGGCAAACAATGAGGGTGCCGAGTGCCTGCGGCTGCTCCAACGAGATCA
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                                                                                 2912 ATCAGICGIGIGAGIGIGIGCTGTIAIGITIGCCICCATIGCCAACTICICGAGIICI
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Patent No. US20020164632a1
GENERAL INFORMATION:
APPLICANT: REPERTON:
TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
FILE REPERENCE: 5800-47
CURRENT APPLICATION NUMBER: US/10/121,911
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/09/412,210
FRIOR APPLICATION NUMBER: US/09/412,210
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (0)...(0)
OTHER INFORMATION: 21529 adenylate cyclase
NAME/KEY: CDS
LOCATION: (247)...(3480)
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US-10-121-911-2
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                                                                                                                  CCGCCAGGACTCCATGTGGGTGGTGAGTAACGTGGTGCTGGCCATCCTGGCGGCAGTGCA
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Length 3518;
Score 505.2; DB 9;
Pred. No. 3.4e-115;
0; Mismatches 1488;
14.2%;
50.0%;
                                            Conservative
                       Similarity
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Query Match
Best Local Sim
Matches 1560;
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1766 2303 1526 1706 1637 1697 1877 2003 2063 2123 2183 2114 2363 2423 1457 1757 1997 2057 2174 2234 2354 2483 2294 2355 CAACCTCTGGGAGCTCCTGGGTCTCTGCCTCTATCAGTGTCCCATACTCATGCA 2414 CTGGGGGGCAGCCAAGCCTTTTGCCCACCTGAGCCACGGAGACAGCCCTGTGTCCACCTC CATGCGCGTGGGCATCCACAGCGGGCGCGTGCACTGCGGGGTCCTTGCGGGAAATG GCAGTTCGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAAGCAGGAAGCCG GGCTGGCCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGT ACCAGGGGGAGTGCACATCACAGGGGCTACCTGGCCCTGGCAGGGGCTTATGCTGT GGAGCCAGGCCGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTT CCTCATCCTGGGCGCCCAGCCAGAAACGCAAAGAGGAGAAAGGCATGCTGGCCAAGCTGCA GCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTT GTCCTCGCTTGAGGGCCTCAAGATGCGTCCATCACTGCTGATGACCCGGTTACCTGGAGTC CTCCCGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGCCATTGATGATTCCAGCAAAGA CAACCGGGGCACCCAAGATGCCCTG+-AACCCTGAGGATGAGGTGGA-TGAGTTCCTGAG CACCCCTCTCCCGGAGAAGACCCTGGCTTCCTTCAGCACCCAGTGGAGCCTGGATCGGAG CCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTTTT CCGTACCCCCCGGGGACTAGATGAACTGGACACCGGGGATGCCAAGTTCTTCCAGGT GCTCACCTTCCAGAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTT CATTGAGCAGCTCGAGAAACAGTGGAAGCAGTCGAAGGACTTCAACCCACTGAC CGGAGCCTACGTTGCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCT ACTGTACTTCAGAGAGAAGGAGATGGAGAAAGAGTACCGACTCTCTGCAATCCCGGCCTT AATTTTCCCACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCT AATCACCGTGCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCA AGTGACAAACAGGCCCCCAGCTCTGGCCATCACG---TATAGCATCACTTTCCTCCTTT ACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTC CGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCAT CAAGATGCTGCACTGCCTGCCTGCACTGTCTGGCCTGGTGGCCACACGACCAGGACTGAG AATAGCCTTGGGCACCACCACCATCCTTGTCTTTGCCATGGCCATTACCAGCCTGTT GCAGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCAC CTTCTTCCCAACATCATCAACACTGCCCTTTCCAAGGTCCCAATGTGTCCTCCATGATTTC CTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTTGGCCAGCTCTGT 1518 1578 1758 1884 1818 1878 2004 1938 1998 2184 2175 1407 1338 1467 1398 1527 1458 1587 1647 1707 1638 1767 1698 1827 1944 2064 2124 2058 2115 2244 2304 2235 2295 2364 2424 g g οy ò δ Q δ Q οχ g Ω a Sy Ob οŽ 95 95 95 QY Db oy Dp g δy OD O.Y Db δ QO g δ

3425 3185 3245 3305 3365 3083 3314 2654 2783 2774 3074 3134 3434 CTTCCTGCACATCAGCACCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGGGCTCATCTA TCTCTACCACCAGTCCTATGAATGCGTTTGTGTCCTCTTCGCCTCAGTCCCAGACTTCAA ATATGACATTGGGGCAACACAGTGAACGTGGACCCGCCGAGCCATGGAGAGTACAGGAGGTCCT GCTGCTGCTGCTGCTGTGGCGGCGATCCTGCTCCTCTTCCTGCACTCCCATGC TGGCGTCCATGGCTTGTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCTGC GTATCTGCATGCTCAGCAGGTGGAATCGACTGCCGCCTAAACTTCCTCTGGAAACTACA cerrerecrescresearsasracracresescresarrererasaa ACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTTATGTTTGCCTCCATTGCCAACTTCTC ------CTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCTGACTACGC CATGCGCCTCATGGAGCAGATGAGCACATGAGCACTCCTTCAACAATTTCCAGAT cereseccresesercrasecresacercarcaacaascarrearcaacaacrresecr GTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACGGGGGGTCCC CGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCT GGAGTGTCGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGGAGATGACCACCTACTTCCTCAA CTGCTGCACGCTGGGCTTCCTCTCCTGCTCCTCTTTCTGCACATGAGCTTCGAGCTGAA TTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTGACAACTATGACCTACTGCT CTGGCTGTCGGAATGCCTCATCGTCCGCCTCTATCTGGGCCCCTTGGACTCCAGGCCCGG AGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTGGTGTTTGCGCTGGCGCT GGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTACAGGCATACAACCGGAGGCTGCTA TAACATTCTGCCCAAGGACGTGGCGGCCCACTTCCTGGCCCGGGAGCGCCCGCAATGATGA TGAGTTCTATGTGGAGCTGGAGGCAAACAATGAGGGTGCCGAGTGCCTGCGGCTGCTCAA CGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGGGGGGTTCCGGCAGCTGGAAAA GATCAAGACGATTGGTAGCACCTACATGGCTGCCTCAGGGCTGAACGCCAGCAC----GGATGCACAACAGGATGCTGAACGGAGCTGCAGCCACCTTGGCACTATGGTGGAATTTGC GAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGGAAGCCACA 2715 2835 3195 3255 3375 2415 2544 2604 2595 2724 2655 2895 2955 3015 3075 3135 3246 3366 3315 3426 2484 2475 2535 2664 2784 2844 3024 3084 3186 2904 2964 3138 3306 g ò q δ Q Qγ q Q Dp oy Db OY Db QY Db OY OY Db 90 y g Oy Db oy Db g δy δ QY Db δŽ g

RESULT 11 US-09-925-297-352

[;] Sequence 352, Application US/09925297 ; Patent No. US20020081659A1

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                                                                                                                                                                                                                                                                                                                                         DB 10; Length 2601;
                  Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                       Score 395.8; DB 10;
Pred. No. 3.8e-88;
1; Mismatches 1143;
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
TITLE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR PLILING DATE: 2000-03-08
PRIOR PLILING DATE: 1999-0312
PRIOR FILING DATE: 1999-0312
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                         NAME/KEY: misc feature

: LOCATTON: (2520)

: OTHER INFORMATION: n equals a,t,g, or

: NAME/KEY: misc feature

: LOCATTON: (2572)

: OTHER INFORMATION: n equals a,t,g, or

US-09-925-297-352
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 51.1%;
Matches 1301; Conservative
                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                      SEQ ID NO 352
LENGTH: 2601
                                                                                                                                                                                     TYPE: DNA
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1161 cccgctactccgfgcagaaggagagagagagaggcgcgccgcctrcagctccrccrccgcgcg 1220 2464 2584 AGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGC 1933 ACCCACGCCGGAGCTGCGCCTGCAGGACCTGGCTGACCGAGTGGTGGATGCCTCTGAAG 1040 1041 ATGAGCACGAGCTCAACCAGCTGCTCAACGAGGCCCTGCTTGAGCGAGAGTCCGCCCAAG 1100 TAGTAAAGAAGAGAAACACCTTCCTTGTCCATGCGGTTCATGGACCCCGAGATGGAA 1160 1221 TCCTGCTCTGCACGCCCTGGTCGAGATACTCATCGACCCCTGGCTAATGACAAACTATG 1280 TGACCTTCATGGTGGGGGAGATTCTGCTCCTCATCCTGACCATCTGCTCCTGGCTGCCA 1340 1401 GCTGGGCCAGGAACACCTGGGCCATGCTCGCCATCTTCATCCTGGTGATGGCAAATGTCG 1460 1575 GGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCA 1634 TGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTC 1753 CTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATG 1813 1814 ATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATG 1873 1341 TCTTTCCCCGGGCCTTTCCTAAGAAGCTTGTGGCCTTCTCAACTTGGATTGACCGGACCC 1400 1461 TGGACATGSTCAGCTGTCTCCAGTACTACACGGGACCCAGCAATGCAACGGCAGGGATGG 1520 1521 AAACGGAGGCAGCTGCCTGGAGAAC---CCCAAGTATTACAACTATGTGGCCGTGCTGT 1577 CCCTCATCGCCACCATCATGCTGGTGCAGGTCAGCCACATGGTGAAGCTCACGCTCATGC 1637 TGCTCGTCGCAGGCGCCGTGGCCACCATCAACCTCTATGCCTGGCGTCCCGTCTTTGATG 1697 AATACGACCACAAGCGTTTTCGGGAGCACGACTTACCTATGGTGGCCTTAGAGCAGATGC 1757 FIGECCTCAAT-----GGCTCGGCCCTGCCCAATGGAGCACCAGCTTCCTCAAAGTCCAG 1991 TGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCT CCGCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCA 1635 CATTGAGACTTTCCTCATCCTGGGCGCC-AGCCAGAAACGGAAAGAGAAAGGCATGC GCCGGTTTTTGCTCACC - - - TTCCAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGG 2051 TCATCCAGCTTCTAATTTTCCCACCTCCACCCTGATGCTTGGGATTTATGCCAGCATCT TGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCACATAGCA CCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACCTGCTG ACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCTGT GTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCCATCGGGAACATGCTGCTGA GTCTCTTGGCCAGCTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCT TTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTG ---GGCTTC ACAACTATGACCTACTGCTTGGCGTCCATGGCTT--1694 1754 1281 694 754 868 981 1101 2111 2165 2225 2405 2465 2525 2585 g g рp Q δ δ g δ g ò 셤 g δ ò g ò g ò δ g ŏ g g δ g g g ŏ

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                                                                                                               2745 GGAATCGACTGCCCGCCTAAACTTCCTCTGGAAACTACAGGCAACAGGGGAAAAAGAGGA 2804
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                                               TATGACCCCTGTGATTCTGCTGTGTTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGT
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APPLICANT: Insel, P. A.
APPLICANT: Ping, P. A.
APPLICANT: Ping, P. A.
APPLICANT: Gao, M.
TILLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TILLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TILLE OF INVENTION: FAILURE
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 1999-12-27
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US-09-750-240-1
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Pred. No. 1.2e-63;
0; Mismatches 9; Indels
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Patent No. US20020120103A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS723P1
CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-17
PRIOR FILING DATE: 2000-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-09-12
NUMBER: PAPLICATION NUMBER: 60/231,968
PRIOR FILING DATE: 2000-09-12
NUMBER: PAPLICATION NUMBER: 50/231,968
PRIOR FILING DATE: 2000-09-12
NUMBER: PAPLICATION NUMBER: 50/231,968
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO! 314
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(314)
CTHER INFORMATION: n = A,T,C or G
US-09-750-240-1
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Best Local Similarity 97.1%;
Matches 300; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                       189 ccGGAGTGCTGAAGGAGCCCAAACTGATGGGTGCTATCTCCTTCTTCATCTTCTTCA 248
                                                                                                                                                                                                               669 GACAGGATGCACAACAGGATGCTGAACGGAGCTGCAGCCACCATGGCACTATGGTGGAAT 728
                                                                                                                                                                                                                                                             2840 IGCATAACATTCTGCCCCAAGGACGTGGCGGCCCACTTCCTGGCCCGGGAGCGCCCGCAATG
                                                                                                                                                                                                                                                                                                            909 TCCTTGGCAAAATCCAAGTGACTGAGGAGACAGCATGGGCCCTACAGTCCCTGGGCTACA
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                                                                                                    Length 1180;
                                                                                                                            Indels
                                                                                                Score 284.4; DB 10;
Pred. No. 1e-60;
0; Mismatches 321;
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                                                              n equals a, t, g, or
NAME/KEY: SITE
LOCATION: (1163)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (1164)
OTHER INFORMATION: n equals a,t,g,
                                                                                               Query Match 8.0%;
Best Local Similarity 59.8%;
Matches 505; Conservative
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2729 TGCATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCCTCTGGAAACTACAGGCAA 2788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1140;
                                                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTIN VET. 2.0
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0; Mismatches 310
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NAME/KEY: misc feature
LOCATION: (1135)
COTHER INFORMATION: n equals a,t,g,
US-09-925-297-56
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                                          Sequence 56, Application US/09925297 Patent No. US20020081659A1
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OTHER INFORMATION: n equals
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LOCATION: (1115)
OTHER INFORMATION: n equals
NAME/KEF: misc feature
LOCATION: (1119)
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Matches 491; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                GENERAL INFORMATION:
APPLICANT: Rosen et al
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RESULT 14
US-09-925-297-56
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LENGTH: 1140
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                                                  3191 GGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGA 3250
                                                                                                                     TTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGGAAGCCACAGTATG 3310
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Pred. No. 2.2e-51;
4; Mismatches 337; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 792, Application US/09764864
Fatent No. US20020132753A1
GENERAL INFORMATION:
FAPLICANT: Rosen et al.
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 792
LENGTH: 7053
                                                                                                                                                                                                                                                                                                                               GTCGAGGGGTGGTC--AAGGTGAAGGGCAAGGGGGAGATGA 3469
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; OTHER INFORMATION: n equals a,t,g, or
US-09-764-864-792
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Best Local Similarity 58.0%;
Matches 497; Conservative 4
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                     TCATCGCTGACTTTGATGAGATTATCAGCGAGGGGGGTTCCGGCAGCTGGAAAGATCA 3088
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                                                                                                                                   6255 ACCAGGAGCTGGAGCGKCAGCATGCCCACATTGGTGTCATGGTGGTGAGTTCAGCATCGCCC
                                                                                                              GCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCTGACTACGCCGTTGCGGC
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BO231940 AGENCOURT
BM943080 UI-W-CGOP
AA207907 mW84h06.r
BG872335 602792616
BB937119 601229307
BM964004 UI-W-EQO-
BM964004 UI-W-EQO-
BM953572 ILZ-NT019
BC935972 ILZ-NT019
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BC935672 ILZ-NT019
BC935672 UI-W-BC094-
BI680978 46-DS-
BC05641 CM-FN010
BC65641 CM-FN010
BC653668 277573 MA
BC840138 QVO-FN018
BC65368 277573 MA
BC840138 QVO-FN018
BC65368 QV4-CN018
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AGENCOURT_6489534 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724057
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F131214 H8C3KC121 n
B181775 UMIGG02
B1257644 602967566
BC028085 H0mo sapi
B173936 603959680
B1257519 602967658
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Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM12712 row: 1 column: 10
High quality sequence stop: 644.
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1 (bases 1 to 1039)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                             BI255147
BQ231940
BM943080
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BM964004
BM090325
AU169950
BQ180663
BF295972
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AI905602
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BE838164
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AW481229
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BE001572
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BE840138
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KEYWORDS
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TITLE
JOURNAL
COMMENT
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BM811640
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BQ881496 AGENCOURT
BF792125 602252571
BE40188 QVO-FN018
BI691747 603307455
BG297229 602394937
                                                                                                       February 28, 2003, 21:14:01; Search time 3408.29 Seconds (without alignments) 16864.108 Million cell updates/sec
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              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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772
718.8
593.4
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Homo sapi 603359680 602967658

602967566

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Query Match
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TITLE
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/clone_Ilp="NIH_MGC_125"
/lab_host="DH108"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: Ecory (destroyed): Site_2: Not!; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dr primed and directionally cloned (Ecory site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
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                                                                                                                                                                                          2 others
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Pred. No. 2e-173;
0; Mismatches 23;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                 Query Match 22.8%;
Best Local Similarity 97.2%;
Matches 833; Conservative
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clone IMAGE:6182035 5', mRNA sequence.
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1 (bases 1 to 1016)

NIH-MGC http://mgc.nci.nih.gov/.
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Contact: Robert Strausberg, Ph.D.
2947
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Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13567 row: f column: 20
High quality sequence start: 31
High quality sequence stop: 645.
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/clone_lib="Lupski_dorsal_root_ganglion"
/sex="male"
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94.1%; Pred. No. 4.8e-165;
ive 0; Mismatches 45;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .775
/ Organism="Homo sapiens"
//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone=InMAGE:4345144"
//clone=Lib="NIH_MGC_84"
//clone_Lib="NIH_MGC_84"
//lssue_Uype="adrenal cortex carcinoma, cell line"
//lab_host="DH10B (phage-resistant)"
//note="Organ: adrenal gland; Vector: pcMV-SPORT6; Site_1:
//note="Organ: adrenal gland; Vect
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                                      cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9964 row: m column: 17
High quality sequence stop: 711.
Location/Qualifiers
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Pred. No. 5.9e-153;
0; Mismatches 12; Indels
                    Tissue Procurement: ATCC
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Local Similarity 98.1%;
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1 (bases 1 to 775)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                             AGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LLCR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVO-FN0181-100
800-335-d08&t3=2000-08-10&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note—"Organ: prostate_normal; Vector: puc18; Site_1: Smal ; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                             BE840188 676 bp mRNA linear EST 22-SEP-2000 QVO-FN0181-100800-335-d08 FN0181 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
  CTAGCTGCCAAGGGCTACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGCAAGGGG 3462

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      GAAGTGGAGCCAGGCCAAGCGCAACGCGTACCTCAAGGAGCACACATTGAG
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202653
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llarity 95.9%; Pred. No. 2.1e-124;
Conservative 0; Mismatches 26;
                                                                                             GAGATGACCACCTACTTCCTCAATGGGGGCCC 3494
                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0181"
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High quality sequence stop: 625.
Location/Qualifiers
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BI691747 12.25 bp mRNA linear EST 18-SEP-2001 603307455F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5343565 5',
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S NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Ph.D.
Contac
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone="IMAGE:5343565"
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                                                  /note="Organ: mammary; vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
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9
                                                                                                                        Query Match 16.2%; Score 573.6; DB 13; Length 1225; Best Local Similarity 87.4%; Pred. No. 8.2e-120; Matches 696; Conservative 0; Mismatches 94; Indels 6;
                       ductal carcinoma"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating di
/dev_stage="5 months"
/lab_host="DH10B"
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BG297229 1043 bp mRNA linear EST 21-FEB-2001 602394937F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4506705 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /close_lbb="NHL_MCC_94"
/tissue_type="retina"
/lab_host="DHIOB (phage-resistant)"
/note="Corgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
full-length clones and constructed by Life Technologies.
295 c 312 g 158 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.ri column: 10
Plate: LLAMI0382 row: i column: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4506705"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 647. Location/Qualifiers
                                                                                                                                 BG297229.1 GI:13060672
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                                                                     mRNA sequence.
                                                                                                                                                                                            house mouse.
Mus musculus
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Gaps

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Indels

87;

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Pred. No. 9.8e-117;
                 0; Mismatches
 87.78;
 Best Local Similarity 87.7
Matches 634; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 743)

I (bases 1 to 743)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the II.M.A.G.E. Consortium/LLNL at:

Http://mage.llnl.gov

Plate: LLAMIBT99 row: j column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                          BI685206 743 bp mRNA linear EST 18-SEP-2001 603310213F1 NCI_CGAP_Mam6 Mus musculus CDNA clone IMAGE:5346147 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                 3430
                                                                                                        3371 GAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGAGT
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                                                                                       3251 TIGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCCTCGGAAGCCACAGTATG
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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Location/Qualifiers
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BI685206
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ORGANISM
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TITLE
JOURNAL
COMMENT
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BI685206
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KEYWORDS
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DB 13; Length 743;

15.8%; Score 559.8;

Query Match

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BG287169 796 bp mRNA linear EST 21-FEB-2001 6023818888F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4499589 5',
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1 (bases 1 to 796)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                2604 TGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCTGC 2663
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2424 CTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGGTGAGTCTCTTGGCCAGCTCTGT
                                                         23 CTGCAGCTTCCCTGAGTACTTCGTCGGGAACGTGCTGCTGAGTCTTCTAGCCAGCTCTGT
                                                                                                                                                                                                                                 2544 TTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTGACAACTATGACCTACTGCT
                                                                                                                                                                                                                                                               143 CTTGGTGCTGTTTTGCTGGTCCCCCGGCCGCCATCTTTGACAACTATGATCTACTGCT
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BG287169.1 GI:13040741
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AUTHORS
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AATTCAGCTTGAAAGGGACCAAGGTGGGCATT
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Best Local
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                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="Inbe=1499589"
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/lab_bost="blidb (phage-resistant)"
/note="Organ: bladder; Vector: pcWV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."

07 a 193 c 245 g 151 trary."
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                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMN0363 row: p column: 22
High quality sequence start: 7
High quality sequence start: 7
Location/Qualifiers
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               Tissue Procurement: ATCC
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97.0%;
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/organism="Homo saplens"
/db_xref="taxon:9606"
/clone_lib="H10999"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
ысэуэлго 581 bp mRNA linear EST 13-JUN-2001
MR3-HT0999-070201-003-h04 HT0999 Homo sapiens CDNA, mRNA sequence.
BG993320
                                                                                                                                                                                                                        Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 581)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-MR3&t2-MR3-HT0999-070201-003-h04&t3=2001-02-07&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 2.6e-112;
0; Mismatches 9;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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High quality sequence stop: 581
Location/Qualifiers
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al Similarity 98.2%;
556; Conservative
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 790)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                                   1556 CACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCAACG 1615
                                                                                                                               AAGAGGAGAAAGGCATGCTGGCCAAGCTGCAGCGGACTCGGGCCCAACTCCATGGAAGGGC 1735
                                                                                          196 TGCACTGCGGCGTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGA 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11298 row: d column: 03
                        1496 CCCTGGCCAACCACATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAA
                                                                                                                                                                                               15.0%; Score 532.4; DB 13; Length 790;
89.9%; Pred. No. 1.7e-110;
.ive 0; Mismatches 61; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 634.
Location/Qualifiers
                                                                                                                                                                                                                                                                                        GCCAGATGGGCATTGATGATTCCAGC 1821
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BI255147
BI255147.1 GI:14808265
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Les 707; Conserv
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bp mRNA linear EST 02-MAY-2002
Homo sapiens cDNA clone IMAGE:6067056
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                    485 AACCGAGATCATCGCTGACTTTCGATGAGATTATCAGGGAGGAGGAGCGGTCCGGCAGCCTG
2542 TATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCGCCATCTTTGACAACTATGACCTACTG
                                                                                                                                                                                                                                                                                                                                          2782 CAGGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTACAGGCATACAACCGGAGGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                              2842 CATAACATTCTGCCCAAGGACGTGGCGGCCCACTTCCTGGCCCGGGAGCGCCGCAATGAT
                                       10 TATTIGGIGCIG-TICTGCIGGGICCCCCAGCCACCATCTTIGACAACTAIGACCIACTG
                                                                                                         2602 CTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCT
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BQ231940
BQ31940.1 GI:20413340
EST.
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2842 CATAACATTCTGCCCAAGGACGTGGCGGCCCACTTCCTGGCCCGGGAGCGCCGCAATGAT 2901
                                                   house mouse.
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                                                                                                                                                                                                                                                                             /tissue_type="embryonal carcinoma, cell line"
/lab_nost="DH10B [phage-resistant,"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
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                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI3345 row: p column: 01
High quality sequence stop: 609.
1. 905
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Pred. No. 6.6e-106;
0; Mismatches 1; Indels 0;
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/db_xref="taxon:9606"
/clone="IMAGE:6067056"
/clone_lib="NIH_MGC_92"
 Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Matches 513; Conservative
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IU-M-CG0p-beo-d-02-0-UI"
/clone="IU-M-CG0p-beo-d-02-0-UI"
/clone="IU-M-CG0p-beo-d-02-0-UI"
/clone="IU-M-CG0p-beo-d-02-0-UI"
/clone="IU-M-CG0p-beo-d-02-0-UI"
/clone="IU-M-Ret4_S2"
/note="Wector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site... Not I; Site... Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraryies at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.ulowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine"
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                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 607)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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Location/Qualifiers
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BM943080
BM943080.1 GI:19402943
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DKFZp761N2323_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
DKFZp761N2323 5', mRNA sequence.
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of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 487)
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6, 14059
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (1972); Email S. Wiemannedkfz- heidelberg. de;
sequenced by GBF (National Research Centre for Blotechnology Ltd
Braunschweig/Germany) within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3022 AACGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAA 3081
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187 TCGGAGTTCTACGTGGAGCTCGAGGCAAACAACGAGGCGTGGAGTGCCTGCGGCTGTT 128
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142 g 102 t
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No sl sequence available.
This clone (DKF2p761N2323) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@trzpd.de.
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/clone_lib="761 (synonym: hamy2)"
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Pred. No. 7.7e-100;
0; Mismatches 1;
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/db_xref="taxon:9606"
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/dev_stage="adult"
/lab_host="DH10B"
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Local Similarity 99.8%;
les 486; Conservative (
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mv84h06.rl GuayWoodford Beier mouse kidney day 7 Mus musculus cDNA clone IMAGE:661787 5' similar to 9b:M93422 Mouse adenylyl cyclase type VI mRNA, complete cds (WOUSE);, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 652)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                         GAGGGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATC
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Tet: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 417.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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/db_xref="taxon:10090"
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                                                                                                                                                                       13.3%; Score 473.2; DB 9; Length 652; llarity 85.8%; Pred. No. 5.1e-97; Conservative 0; Mismatches 88; Indels 1
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Mus musculus
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Contact: Robert Strausberg, Ph.D.
Email: capabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genemics, Inc.
Clone distribution: MGC. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10845 row: p column: 03
High quality sequence stor: 11
High quality sequence stor: 555.
Location/Qualifiers
I. 565
/organism="Mus musculus"
//db.w.of="FVBNN"
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ATAATGTCAGCATCCTGTTTGCGGACATTGAGGGCTTCACCAGCCTGGCCTCCCAGTGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: salivary gland; Vector: pcMv-SPORT6; Si NotI; Site_2: Sali; Cloned unidirectionally. Primer: dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                           NIH'MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGCCATCTCGCTACGTACGTCAGGTCACAGGTGTGAATGTGAACATGCGCGTGGGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAGACATCAACACAAAAAAAGAGGACATGATGTTCCATAAGATCTACATCCAGAAGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 463.4; DB 12; Length 565;
Pred. No. 8.3e-95;
0; Mismatches 46; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4923890"
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (Tl phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.1%;
Best Local Similarity 91.2%;
Matches 515; Conservative 0
```

Search completed: March 1, 2003, 03:52:47 Job time: 3447.62 secs